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54 New tissue plasminogen activator.

57 This invention discloses a new tissue plasminogen activator which has strong activity for converting plasminogen into plasmin that degrades the fibrin network of blood clot to form soluble products and therefore is useful as a thrombolytic agent, a DNA sequence encoding amino acid sequence of it, a process for producing it and a pharmaceutical composition comprising it.

EP 0 302 456 A1

NEW TISSUE PLASMINOGEN ACTIVATOR

This invention relates to a new tissue plasminogen activator. More particularly, it relates to a new tissue plasminogen activator which has strong activity for converting plasminogen into plasmin that degrades the fibrin network of blood clot to form soluble products and therefore is useful as a thrombolytic agent, to DNA sequence encoding amino acid sequence of it, to a process for producing it and pharmaceutical composition comprising it.

The whole amino acid sequence and structure of a native human "tissue plasminogen activator" (hereinafter referred to as "t-PA") and DNA sequence coding for it derived from a human melanoma cell (Bowes) have already been clarified by recombinant DNA technology [Cf. Nature 301, 214 (1983)].

However, the native t-PA obtained by expressing DNA encoding amino acid sequence of the native t-PA in *E. coli* can hardly be refolded and therefore only an extremely small quantity of the active t-PA can be recovered from the cultured cells of the *E. coli*.

From the results of various investigations, inventors of this invention succeeded in producing new t-PA which is well refolded, even in a form of the resultant product obtained from the *E. coli* cells to give an active t-PA, and display a longer half-life and has a stronger thrombolytic activity than the native t-PA.

The new t-PA of this invention may be represented by the following amino acid sequence (I) as its primary structure.

	180		190
20	R-GluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSer		
	200		210
	LeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysVal		
	220		230
25	TyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArg		
	240		250
	AsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrp		
30	260		270
	GluTyrCysAspValProSerCysSerThrCysGlyLeuArgGln		Y
	277	280	290
35	X-GlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIle		
	300		310
	PheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSer		
	320		330
40	SerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeu		
	340		350
	ThrValIleLeuGlyArgThrTyrArgValValProGluGluGluGluGlnLysPheGlu		
45	360		370
	ValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAla		

380 390
 LeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThr
 5 400 410
 ValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGly
 420 430
 10 TyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisVal
 440 450
 ArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAsp
 15 460 470
 AsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAla
 480 490
 CysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuVal
 20 500 510
 GlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLys
 520 527
 25 ValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro

92 100
 30 wherein R is Ser- or CysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrp
 110 120
 SerThrAlaGluSerGlyAlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLys
 130 140
 35 ProTyrSerGlyArgArgProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCys
 150 160
 ArgAsnProAspArgAspSerLysProTrpCysTyrValPheLysAlaGlyLysTyrSer
 40 170 174
 SerGluPheCysSerThrProAlaCysSer-

45 X is -Lys-, -Ile- or bond and

Y is -TyrSerGlnProGlnPheArgIle-, -TyrSerGlnProGlnPheAspIle-, -TyrSerGlnProIleProArgSer- or -ThrLeuArgProArgPheLysIle-.

[The numbering of the amino acid sequences of the t-PA is according to that described in Nature 301, 217 (1983)]

50 In the above amino acid sequence, Asn¹⁸⁴, Asn²¹⁸ and Asn⁴⁴⁸ may be glycosylated depending on the nature of host cellular environment in the process for the preparation thereof by recombinant DNA technology.

In this specification, the following code names are conveniently employed for the new t-PAs of this invention.

55

TTktPA

In the above amino acid sequence (I), R is Ser-, X is -Lys- and Y is -TyrSerGlnProGlnPheArglle-.

TTitPA

In the above amino acid sequence (I), R is Ser-, X is -Ile- and Y is -TyrSerGlnProGlnPheArglle-.

TQitPA

In the above amino acid sequence (I), R is the residues labelled Cys³² to Ser¹⁷⁴- of the native tPA, X is -Ile- and Y is -TyrSerGlnProGlnPheArglle-.

TQktPA

In the above amino acid sequence (I), R is the residues labelled Cys³² to Ser¹⁷⁴- of the native tPA, X is -Lys- and Y is -TyrSerGlnProGlnPheArglle-.

STTktPA

In the above amino acid sequence (I), R is Ser-, X is -Lys- and Y is -TyrSerGlnProGlnPheAsplle-.

STQktPA

In the above amino acid sequence (I), R is the residues labelled Cys³² to Ser¹⁷⁴- of the native tPA, X is -Lys- and Y is -TyrSerGlnProGlnPheAsplle-.

STQitPA

In the above amino acid sequence (I), R is the residues labelled Cys³² to Ser¹⁷⁴ of the native tPA, X is -Ile- and Y is -TyrSerGlnProGlnPheAsplle-.

thTTtPA

In the above amino acid sequence (I), R is Ser-, X is bond and Y is -TyrSerGlnProGlnProArgSer-

uTTtPA

In the above amino acid sequence (I), R is Ser-, X is -Lys- and Y is -ThrLeuArgProArgPheLyslle-

The native t-PA is a single chain serine protease which is converted to a 2-chain form, heavy and light chains, linked by single disulfide bond with plasmin. The light chain (L) is a protease domain and therefore contains the active-site of the enzyme. The heavy chain (H) has a finger domain (F) (having homology to fibronectin), a growth factor domain (E) (homologous to epidermal growth factor) and two kringles (i.e. kringle 1 and kringle 2 domains; K₁ and K₂) having triple disulfide bonds. Accordingly, the native t-PA is composed of five functional domains F, E, K₁, K₂ and L [Cf. European Patent Application laid open No. 0196920 and Proc. Natl. Acad. Sci. USA 83 4670 (1986)].

Therefore, it is to be understood that this invention also provides

(1) finger and growth factor domains lacking t-PA without glycosylation and

(2) finger and growth factor domains lacking t-PA essentially free from other proteins of human and animal origin.

The above-defined t-PA includes t-PA essentially consisting of kringle 1 and kringle 2 domains of the heavy chain and the light chain of the native t-PA, and a t-PA prepared by deletion or substitution of the amino acid sequence of said t-PA (e.g. t-PA essentially consisting of kringle 2 domain of the heavy chain and the light chain of the native t-PA, the above-exemplified t-PAs in which Lys²⁷⁷ is substituted with Ile²⁷⁷, and/or Arg²⁷⁵ is substituted with Gly²⁷⁵, Glu²⁷⁵, Asp²⁷⁵, etc.).

The new t-PA of this invention can be prepared by recombinant DNA technology and polypeptide synthesis.

Namely, the new t-PA of this invention can be prepared by culturing a host cell transformed with an expression vector comprising DNA encoding an amino acid sequence of the new t-PA in a nutrient medium, and recovering the new t-PA from the cultured broth.

In the above process, particulars of which are explained in more detail as follows.

The host cell may include a microorganism [bacteria (e.g. *Escherichia coli*, *Bacillus subtilis*, etc.), yeast (e.g. *Saccharomyces cerevisiae*, etc.)], cultured human and animal cells (e.g. CHO cell, L929 cell, etc.) and cultured plant cells. Preferred examples of the microorganism may include bacteria, especially a strain belonging to the genus *Escherichia* (e.g. *E. coli* HB 101 ATCC 33694, *E. coli* HB 101-16 FERM. BP-1872, *E. coli* 294 ATCC 31446, *E. coli* x 1776 ATCC 31537, etc.), yeast, animal cell lines (e.g. mouse L929 cell, Chinese hamster ovary (CHO) cell, etc.) and the like.

When the bacterium, especially *E. coli* is used as a host cell, the expression vector is usually comprising at least promoter-operator region, initiation codon, DNA encoding the amino acid sequence of the new t-PA, termination codon, terminator region and replicatable unit. When yeast or animal cell is used as host cell, the expression vector is preferably composed of at least promoter, initiation codon, DNA encoding the amino acid sequence of the signal peptide and the new t-PA and termination codon and it is possible that enhancer sequence, 5'- and 3'-noncoding region of the native t-PA, splicing junctions, polyadenylation site and replicatable unit are also inserted into the expression vector.

The promoter-operator region comprises promoter, and Shine-Dalgarno (SD) sequence (e.g. AAGG, etc.) Examples of the promoter-operator region may include conventionally employed promoter-operator region (e.g. lactose-operon, PL-promoter, trp-promoter, etc.) and the promoter for the expression of the new t-PA in mammalian cells may include HTLV-promoter, SV40 early or late-promoter, LTR-promoter, mouse metallothionein I (MMT)-promoter and vaccinia-promoter.

Preferred initiation codon may include methionine codon (ATG).

The DNA encoding signal peptide may include the DNA encoding signal peptide of t-PA.

The DNA encoding the amino acid sequence of the signal peptide or the new t-PA can be prepared in a conventional manner such as a partial or whole DNA synthesis using DNA synthesizer and/or treatment of the complete DNA sequence coding for native or mutant t-PA inserted in a suitable vector (e.g. pTPA21, pTPA25, pTPA102, p51H, pN53, pST112, etc.) obtainable from a transformant (e.g. *E. coli* LE 3921 (pTPA21), *E. coli* JA 221 (pTPA 25) ATCC 39808, *E. coli* JA 221 (pTPA 102) (Lys 277 → Ile) ATCC 39811, *E. coli* JM109(p51H) FERM P-9774, *E. coli* JM109(pN53) FERM P-9775, *E. coli* DH-1(pST112) FERM BP-1966, etc.), or genome in a conventional manner (e.g. digestion with restriction enzyme, dephosphorylation with bacterial alkaline phosphatase, ligation using T4 DNA ligase).

The termination codon(s) may include conventionally employed termination codon (e.g. TAG, TGA, etc.).

The terminator region may contain natural or synthetic terminator (e.g. synthetic fd phage terminator, etc.).

The replicatable unit is a DNA sequence capable of replicating the whole DNA sequence belonging thereto in the host cells and may include natural plasmid, artificially modified plasmid (e.g. DNA fragment prepared from natural plasmid) and synthetic plasmid and preferred examples of the plasmid may include plasmid pBR 322 or artificially modified thereof (DNA fragment obtained from a suitable restriction enzyme treatment of pBR 322) for *E. coli*, plasmid pRSVneo ATCC 37198, plasmid pSV2dhfr ATCC 37145 plasmid pDBPV-MMTneo ATCC 37224, plasmid pSV2neo ATCC 37149 for mammalian cell.

The enhancer sequence may include the enhancer sequence (72 bp) of SV40.

The polyadenylation site may include the polyadenylation site of SV40.

The splicing junction may include the splicing junction of SV40.

The promoter-operator region, initiation codon, DNA encoding the amino acid sequence of the new t-PA, termination codon(s) and terminator region can consecutively and circularly be linked with an adequate replicatable unit (plasmid) together, if desired using an adequate DNA fragment(s) (e.g. linker, other restriction site, etc.) in a conventional manner (e.g. digestion with restriction enzyme, phosphorylation using

T4 polynucleotide kinase, ligation using T4 DNA-ligase) to give an expression vector. When mammalian cell line is used as a host cell, it is possible that enhancer sequence, promoter, 5'-noncoding region of the cDNA of the native t-PA, initiation codon, DNA encoding amino acid sequences of the signal peptide and the new t-PA, termination codon(s), 3'-noncoding region, splicing junctions and polyadenylation site are consecutively and circularly be linked with an adequate replicatable unit together in the above manner.

The expression vector can be inserted into a host cell. The insertion can be carried out in a conventional manner (e.g. transformation including transfection, microinjection, etc.) to give a transformant including transfectant.

For the production of the new t-PA in the process of this invention, thus obtained transformant comprising the expression vector is cultured in a nutrient medium.

The nutrient medium contains carbon source(s) (e.g. glucose, glycerine, mannitol, fructose, lactose, etc.) and inorganic or organic nitrogen source(s) (e.g. ammonium sulfate, ammonium chloride, hydrolysate of casein, yeast extract, polypeptone, bactotrypton, beef extracts, etc.). If desired, other nutritious sources [e.g. inorganic salts (e.g. sodium or potassium biphosphate, dipotassium hydrogen phosphate, magnesium chloride, magnesium sulfate, calcium chloride), vitamins (e.g. vitamin B1), antibiotics (e.g. ampicillin) etc.] may be added to the medium. For the culture of mammalian cell, Dulbecco's Modified Eagle's Minimum Essential Medium(DMEM) supplemented with fetal calf serum and an antibiotic is often used.

The culture of transformant may generally be carried out at pH 5.5 - 8.5 (preferably pH 7 - 7.5) and 18 - 40 °C (preferable 25 - 38 °C) for 5 - 50 hours.

When a bacterium such as *E. coli* is used as a host cell, thus produced new t-PA generally exists in cells of the cultured transformant and the cells are collected by filtration or centrifugation, and cell wall and/or cell membrane thereof are destroyed in a conventional manner (e.g. treatment with super sonic waves and/or lysozyme, etc.) to give debris. From the debris, the new t-PA can be purified and isolated in a conventional manner as generally employed for the purification and isolation of natural or synthetic proteins [e.g. dissolution of protein with an appropriate solvent (e.g. 8M aqueous urea, 6M aqueous guanidium salts, etc.), dialysis, gel filtration, column chromatography, high performance liquid chromatography, etc.]. When the mammalian cell is used as a host cell, the produced new t-PA is generally exist in the culture solution. The culture filtrate (supernatant) is obtained by filtration or centrifugation of the cultured broth. From the culture filtrate, the new t-PA can be purified in a conventional manner as exemplified above.

It may be necessary to obtain the active t-PA from the cell debris of bacteria in the above case. For refolding of thus produced new t-PA, it is preferably employed a dialysis method which comprises, dialyzing a guanidine or urea solution of the new t-PA in the presence of reduced glutathione (GSH) and oxidized glutathione (GSSG) at the same concentration of glutathiones inside and outside of semipermeable membrane at 4 - 40 °C for 2 - 60 hours. In this method, the concentration of the glutathiones is preferably more than 2mM and the ratio of reduced glutathione and oxidized glutathione is preferably 10:1. Further, the glutathiones can be replaced with cysteine and cystine in this method. These method can be preferably used for refolding of all the t-PA including native t-PA produced by DNA recombinant technology.

The new t-PA of this invention is useful as a thrombolytic agent for the treatment of vascular diseases (e.g. myocardial infarction, stroke, heart attack, pulmonary embolism, deep vein thrombosis, peripheral arterial occlusion, etc.). The new t-PA of this invention in admixture with pharmaceutically acceptable carriers can be parenterally to mammals including human being in a form of a pharmaceutical composition such as infusion.

The pharmaceutically acceptable carriers may include various organic or inorganic carrier materials conventionally employed in the preparation of pharmaceutical composition comprising a peptide or protein (e.g. serum albumin etc.).

A dosage of the new t-PA of this invention is to be varied depending on various factors such as kind of diseases, weight and/or age of a patient, and further the kind of administration route.

The optimal dosage of the new t-PA of this invention is usually selected from a dose range of 0.1 - 10mg/kg/day by injection or by infusion.

The total daily amount mentioned above may divisionally be given to the patient for several hours.

Mono(or di, or tri)mer (of oligonucleotides) can be prepared by, for examples the Hirose's method [Cf. Tanpakushitsu Kakusan Kohso 25, 255 (1980)] and coupling can be carried out, for examples on cellulose or polystyrene polymer by a phosphotriester method [Cf. Nucleic Acid Research, 9 1691 (1981), Nucleic Acid Research 10, 1755 (1982)].

Brief explanation of the accompanying drawings is as follows:

Figure 1 shows construction and cloning of plasmid pHVBB.

Figure 2 shows construction and cloning of plasmid pCLiPAxtrp.

Figure 3 shows DNA sequence of BgIII DNA fragment (1974 bp).

Figure 4 shows construction and cloning of plasmid pCLiPAΔxtrp.
 Figure 5 shows construction and cloning of plasmid pTQiPAΔtrp.
 Figure 6 shows construction and cloning of plasmid pTA9004.
 Figure 7 shows construction and cloning of plasmid pTTkPAΔtrp.
 5 Figure 8 shows DNA sequence of EcoRI DNA fragment (472 bp) and
 Figure 9 shows construction and cloning of pTTiPAΔtrp.
 Figure 10 shows construction and cloning of plasmid pTQkPAΔtrp.
 Figure 11 shows construction and cloning of plasmid pMH9003.
 Figure 12 shows construction and cloning of plasmid pSTTktrp.
 10 Figure 13 shows construction and cloning of plasmid pZY.
 Figure 14 shows construction and cloning of plasmid pSTQitrp.
 Figure 15 shows construction and cloning of plasmid pSTQktrp.
 Figure 16 shows construction and cloning of plasmid pMH9006.
 Figure 17 shows construction and cloning of plasmid pthTTtrp.
 15 Figure 18 shows construction and cloning of plasmid pMH9007.
 Figure 19 shows construction and cloning of plasmid puTTtrp.
 Figure 20 shows construction and cloning of plasmid pST118.
 Figure 21 shows cDNA sequence of a native t-PA in pST112.
 Figure 22 shows construction and cloning of plasmid pmTQk118.
 20 Figure 23 shows construction and cloning of plasmid pmTQk112.
 Figure 24 shows construction and cloning of plasmid pHS9006.
 Figure 25 shows construction and cloning of plasmid pHS3020.
 Figure 26 shows construction and cloning of plasmid pmTTk.
 Figure 27 shows construction and cloning of plasmid pMH3025.
 25 Figure 28 shows construction and cloning of plasmid pmSTTk.
 Figure 29 shows DNA sequence of coding region in pTTkPAΔtrp.
 Figure 30 shows DNA sequence of coding region in pTTiPAΔtrp.
 Figure 31 shows DNA sequence of coding region in pTQkPAΔtrp.
 Figure 32 shows DNA sequence of coding region in pTQiPAΔtrp.
 30 Figure 33 shows DNA sequence of coding region in pSTTktrp.
 Figure 34 shows DNA sequence of coding region in pSTQktrp.
 Figure 35 shows DNA sequence of coding region in pSTQitrp.
 Figure 36 shows DNA sequence of coding region in puTTtrp.
 Figure 37 shows DNA sequence of coding region in pthTTtrp.
 35 Figure 38 shows DNA sequence of coding region in pmTQk112.
 Figure 39 shows DNA sequence of coding region in pmTTk.
 Figure 40 shows DNA sequence of coding region in pmSTTk.

The following Examples are give for the purpose of illustrating this invention, but not limited thereto.

In the Examples, all of the used enzymes (e.g. restriction enzyme, bacterial alkaline phosphatase, T4
 40 DNA ligase) are commercially available and conditions of usage of the enzymes are obvious to the person
 skilled in the art, for examples, referring to a prescription attached to commercially sold enzymes.

Example 1 (Synthesis of oligonucleotides)

The following oligonucleotides were prepared in a conventional manner described as mentioned above.

1) For pHVBB

(HindIII) (EcoRV) (BglIII) (BamHI)

LysLeuGlnAspIleGluGlyArgSer

← HP10 → ← PH7 →

AGCTTCAGGATATCGAAGGTAGATCTG

AGTCCTATAGCTTCCATCTAGACCTAG

← HP11 → ← HP9 →

HP10; AG-CTT-CAG-GAT

HP7 ; ATC-GAA-GGT-AGA-TCT-G

HP11; C-GAT-ATC-CTG-A

HP9 ; GA-TCC-AGA-TCT-ACC-TT

2) For pTQiPAΔtrp and pTQkPAΔtrp

(ClaI) ^fMetCys¹TyrGlu (AvaII)

← HP23 → ← HP24 →

CGATAAAATGTGTTATGAG

TATTTTACACAATACTCCTG

← HP25 → ← HP26 →

HP23; C-GAT-AAA-AT

HP24; G-TGT-TAT-GAG

HP25; ACA-CAT-TTT-AT

HP26; GTC-CTC-ATA

Cys¹ of TQiPA or TQkPA is corresponding to Cys³² of the native t-PA reported in Nature 301, 214 (1983).

HP31; C-GAT-AAA-ATG-TC

Example 4 (Construction and cloning of plasmid pCLiPAΔxtrp)
(as illustrated in Fig. 4)

pCLiPAxtrp was digested with BamHI and SacI and the resultant 5388 bp DNA fragment was isolated.
5 On the other hand, pCLiPAxtrp was digested with Sau3AI and SacI. The resultant 389 bp DNA fragment was ligated to the 5388 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pCLiPAΔxtrp (5777 bp) was isolated and was characterized by restriction endonuclease (ClaI, EcoRI, XhoI, NarI and SacI) digestion.

Example 5 (Construction and cloning of plasmid pTQiPAΔtrp)
(as illustrated in Fig. 5)

15 pTPA102 (Lys²⁷⁷ → Ile) as mentioned above was digested with AvaI and BbeI, an isoshizomer of NarI creating 4 nucleotide-long single-stranded cohesive terminal, and the resulting 50 bp DNA fragment encoding Asp⁹⁵ - Ala¹¹¹ of the native t-PA was isolated. On the other hand, the synthetic 19 bp ClaI - AvaI DNA fragment was prepared from HP23, HP24, HP25 and HP26(see:Example 1) using T4 polynucleotide kinase and T4 DNA ligase. It was ligated to the 50 bp DNA fragment with T4 DNA ligase to construct the 69
20 bp ClaI - BbeI DNA fragment.

pCLiPAΔxtrp was linearized by BbeI partial digestion. The resultant 5777 bp DNA fragment was digested with ClaI and the 5149 bp DNA fragment was isolated. It was ligated to the 69 bp ClaI - BbeI DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pTQiPAΔtrp (5218 bp) was obtained.
25 which was characterized by restriction endonuclease digestion.

E. coli HB101-16 [recA⁻, supE⁻, htrR16(am), tet^r] FERM P-9502] was transformed with pTQiPAΔtrp to give a transformant, E. coli HB101-16 (pTQiPAΔtrp).

30 Example 6 (Construction and cloning of plasmid pTA9004)
(as illustrated in Fig. 6)

pCLiPAΔxtrp was digested with DdeI and EcoRI and the 91 bp DNA fragment encoding Glu¹⁷⁵ Trp²⁰⁴ of the native t-PA was isolated. The resultant DNA was ligated to oligodeoxyribonucleotides HP31 and
35 HP32(see:Example 1-(3)) using T4 polynucleotide kinase and T4 DNA ligase. The resultant 103 bp ClaI - EcoRI DNA fragment was ligated to the 4397 bp ClaI - EcoRI fragment of pCLiPAΔxtrp in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pTA9004 (4500 bp) was obtained.

40 Example 7 (Construction and cloning of plasmid pTTkPAΔtrp)
(as illustrated in Fig. 7)

pTA9004 was digested with EcoRI and the resultant DNA fragment (4500 bp) was dephosphorylated
45 with bacterial alkaline phosphatase. On the other hand, pTPA21 which comprises the complete cDNA sequence encoding the native t-PA and a portion of the 3'-noncoding region was digested with EcoRI and the 472 bp DNA fragment encoding Asn²⁰⁵ - Lys³⁵¹ of the native t-PA (DNA sequence of which is shown in Fig. 8) was isolated. The resultant DNA fragment was ligated to the dephosphorylated 4500 bp EcoRI DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From
50 one of the ampicillin resistant transformants, the desired plasmid pTTkPAΔtrp (4972 bp) was isolated. E. coli HB 101-16 was transformed with pTTkPAΔtrp to give a transformant E. coli HB101-16 (pTTkPAΔtrp).

Example 8 (Construction and cloning of plasmid pTTiPAΔtrp)
55 (as illustrated in Fig. 9)

pTA9004 was digested with EcoRI and the resultant DNA was dephosphorylated with bacterial alkaline phosphatase. On the other hand, pTPA 102 (Lys²⁷⁷ → Ile) as mentioned above was digested with EcoRI

and the 472 bp DNA fragment encoding Asn²⁰⁵ - Lys³⁶¹ of the mutant t-PA (Lys²⁷⁷ → Ile) was isolated. The resultant DNA fragment was ligated to the dephosphorylated 4500 bp EcoRI DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pTTiPAΔtrp (4972 bp) was isolated. E. coli HB101-16 was transformed with pTTiPAΔtrp to give a transformant E. coli HB 101-16 (pTTiPAΔtrp).

Example 9 (Expression and isolation)

A single colony of E. coli HB 101-16 (pTTkPAΔtrp) was inoculated into 5 ml of sterilized L.A broth containing bactotrypton 10 g, yeast extract 5 g, NaCl 5 g, 50μg/ml ampicillin (pH 7.2 - 7.4) in a test tube and incubated at 37°C for 8 hours under shaking condition. The cultured broth was added to 100 ml of sterilized fresh LA broth in a flask and incubated at 37°C for 15 hours under shaking condition. A portion (20 ml) of the resultant broth was added to 400 ml of sterilized M9CA broth containing 25μg/ml ampicillin, and the mixed broth was incubated at 37°C. When A₆₀₀ of the broth reached approximately 0.6, β-indoleacrylic acid was added to the broth in a final concentration of 10μg/ml. The resultant broth was incubated at 37°C for 3 hours, and centrifuged at 4°C, 8, 900 x g for 10 minutes. The harvested cells were suspended in 100 ml of 10 mM Tris-HCl (pH 8.0) containing 5 mM EDTA, and treated with 50 mg of lysozyme at 4°C for 1 hour. The resultant mixture was homogenized by a Biotron blender and centrifuged at 4°C, 8, 900 x g for 30 minutes. The pellets were washed with 100 ml of 50% aqueous glycerol and dissolved in 800 ml of 10 mM Tris-HCl (pH 8.0) containing 8M urea. To the urea solution, 480 mg of GSH (Kojin) and 96 mg of GSSG (Kojin) were added. The resultant mixture was dialyzed twice against 16 liters of a buffer solution (pH 9.5) containing 20 mM acetic acid, 40 mM ammonia, 2 mM GSH and 0.2 mM GSSG at 4°C for 15 hours. After centrifuging the mixture, the supernatant was assayed by the following fibrin plate assay. The fibrin plate assay (FPA) was carried out according to the method [Astrup T. and Müllertz S., Arch. Biochem. Biophys. 40 346 - 351 (1952)] with minor modification. A fibrin plate was prepared by mixing 5 ml of 1.2% human plasminogen-rich fibrinogen (Green - Cross) in 100 mM phosphate buffer (pH 7.2) with 5 ml of thrombin (Mochida, 50 units) in the same buffer, followed by allowing to stand at room temperature for 1 hour. The test solution or human native t-PA (WHO standard) (10 μl of each) were incubated at 37°C for 18 hours. Using the human native t-PA as the standard, the activities of the samples were calculated from the areas of the lysis zones. From the result of assay, the t-PA activity of the supernatant containing TTkPA was 2.3 x 10⁵ IU of the native t-PA/l.

Example 10 (Expression and isolation)

A single colony of E. coli HB 101-16 (pTTiPAΔtrp) was cultured and TTiPA was isolated from the resultant cultured broth in the substantially the same manner as that described in Example 9. The t-PA activity of the resultant supernatant containing TTiPA was 2.0 x 10⁴ IU of the native t-PA/l.

Example 11 (Expression and isolation)

A single colony of E. coli HB 101-16 (pTQiPAΔtrp) was cultured and TQiPA was isolated from the resultant cultured broth in the substantially the same manner as that described in Example 9. The t-PA activity of the resultant supernatant containing TQiPA was 2.0 x 10⁴ IU of the native t-PA/l.

Example 12 (Purification of TTktPA)

All procedures were performed in cold room (at 4 - 6°C). The plasminogen activator, TTktPA in the supernatant renatured was isolated and purified as follows:

In the first step, the supernatant prepared from 20 liter of the cultured broth obtained in a similar manner to that described in Example 9 [TTktPA total activity: 3.4 x 10⁶ IU of the native t-PA (WHO)] was loaded onto benzamidine Sepharose column [1.6 cm x 3 cm : p-aminobenzamidine was linked covalently to CH Sepharose 4B (Pharmacia) by the carbodiimide method described in the literature : Las Holmberg, et al., BBA, 445, 215 - 222 (1976)] equilibrated with 0.05 M Tris-HCl (pH 8.0) containing 1M NaCl and 0.01% (v/v) Tween80 and then washed with the same buffer. The plasminogen activator was eluted with 0.05M

Tris-HCl (pH 8.0) containing 1M arginine and 0.01% (v/v) Tween80.

In the next step, pooled active fractions were applied on IgG coupled Sepharose (FTP 1163) column (1.6 cm x 3 cm) [monoclonal anti t-PA antibody: FTP 1163 (Tsutomu Kaizu et al., Thrombosis Research, 40 91 - 99 (1985) was coupled to CNBr activated Sepharose 4B according to manufacture's instructions] equilibrated with 0.1 M Tris-HCl (pH 8.0). The column was washed with 0.1 M Tris-HCl (pH 8.0) containing 1M NaCl, 0.01% (v/v) Tween80 and Aprotinin (10 KIU/ml, Sigma). Elution was done with 0.1M glycine-HCl (pH 2.5) containing 0.5 M NaCl, 0.01% Tween80 and Aprotinin (10 KIU/ml).

In the last step, pooled active fractions obtained from the IgG Sepharose (FTP1163) column were dialyzed against 1 liter of 0.01 M phosphate buffer (pH 7.4) containing 1.6 M KSCN and 0.01% (v/v) Tween80. The solution dialyzed was concentrated to about 2 ml by dialysis against solid polyethylene glycol 20,000. The concentrate obtained was gel-filtered on a Sephacryl S200HR (Pharmacia, 1.6 cm x 90 cm) in 0.01 M phosphate buffer (pH 7.4) containing 1.6 M KSCN and 0.01% (v/v) Tween80. The pooled active fractions were concentrated to about 10 ml by dialysis against solid polyethylene glycol 20,000 and the concentrate was then dialyzed against 0.1 M ammonium bicarbonate containing 0.15 M NaCl and 0.01% (v/v) Tween80 to give dialyzate containing purified TTktPA (3.4 mg, 7.35×10^5 IU of the native t-PA (WHO)-mg*protein).

The TTktPA purified have following characteristics.

(i) Analytical SDS PAGE

A 15% polyacrylamide gel was prepared according to the method of Laemmli (U.K. Laemmli, Nature (London) 227, 680 - 685 (1970)). The gel was stained with silver (H.M. Poehling, et al., Electrophoresis, 2, 141 (1981)).

TTktPA thus purified migrate on the SDS-PAGE as a single band at 35K Daltons under reducing condition and 32K Daltons under nonreducing condition, whereas material incubated with plasmin Sepharose (Per Wallin, et al., BBA, 719, 318 - 328 (1982)) yielded two bands at 30K Daltons (protease domain) and 13.5K Daltons (kringle domain) in the presence of reducing agent, and only one band at 32K Daltons in the absence of reducing agent.

(ii) HPLC

TTktPA purified was applied to a (4.6 mm x 75 mm) ultrapore RPSC column (Beckman, USA). Elution was performed with a linear gradient of acetonitrile (10 - 60% (v/v) in 0.1% (v/v) trifluoroacetic acid at a flow rate of 1.0 ml/min over 30 minutes.

In this system, TTktPA was eluted as single major species at an acetonitrile concentration of approximately 36.5% (v/v).

(iii) N-terminal sequence analysis

Purified single chain TTktPA was reduced and carboxymethylated, desalted on HPLC (Ultrapore RPSC column, concentrated by Speed Vac Concentrator (Savant) and analyzed using a gas phase sequencer, model 370A (Applied Biosystem). The N-terminal amino acid sequence of thus obtained TTktPA was as follows.

SerGluGlyAsn -

Example 13 (Construction and cloning of plasmid pTQkPAΔtrp) (as illustrated in Fig. 10)

The plasmid pTQkPAΔtrp was digested with EcoRI. The reaction mixture was dephosphorylated with bacterial alkaline phosphatase and the resultant 4744 bp DNA fragment was isolated. On the other hand, the plasmid pTPA 21 was digested with EcoRI and the resultant 472 bp DNA fragment was isolated. The 472

bp DNA fragment was ligated to the 4744bp DNA fragment in the presence of T4 DNA ligase and the ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pTQkPA Δ trp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with the plasmid pTQkPA Δ trp to give a transformant E. coli HB101-16 (pTQkPA Δ trp).

Example 14 (Synthesis of oligonucleotides)

The following oligonucleotides were prepared in a conventional manner described as mentioned above.

- 1) Linkage sequence for pSTTktrp and pSTQktrp
(DdeI) (EcoRV) (StuI)

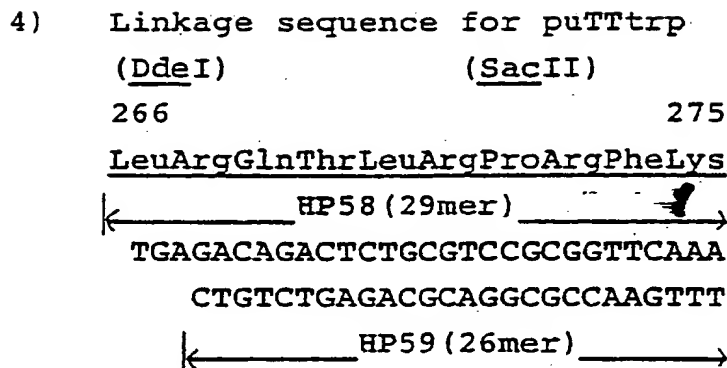
266 270 275
LeuArgGlnTyrSerGlnProGlnPheAspIleLysGlyGly
|----- SK1 (40mer) -----|
TGAGACAGTACAGCCAGCCACAGTTTGATATCAAAGGAGG
CTGTTCATGTCGGTCGGTGTCAAACCTATAGTTTCCTCC
|----- SK2 (37mer) -----|

- 2) Linkage sequence for pSTQitrp
(DdeI) (EcoRV) (StuI)

266 270 275
LeuArgGlnTyrSerGlnProGlnPheAspIleIleGlyGly
|----- HP56 (40mer) -----|
TGAGACAGTACAGCCAGCCACAGTTTGATATCATAGGAGG
CTGTTCATGTCGGTCGGTGTCAAACCTATAGTATCCTCC
|----- HP57 (37mer) -----|

- 3) Linkage sequence for pthTTtrp
(DdeI) (BglIII) (StuI)

266 275
LeuArgGlnTyrSerGlnProIleProArgSerGlyGly
|----- HP60 (37mer) -----|
TGAGACAGTACAGCCAGCCAATTCCTAGATCTGGAGG
CTGTTCATGTCGGTCGGTTAAGGATCTAGACCTCC
|----- HP61 (34mer) -----|



Numbers above the amino acids refer to the positions of the native t-PA reported by Pennica et al - (Nature 301 214-221, 1983).

Example 15 (Construction and cloning of plasmid pMH9003)
(as illustrated Fig. 11).

The plasmid pTA9004 was digested with EcoRI and StuI, and the resultant 4329 bp DNA fragment was isolated. The DNA fragment was ligated to the synthetic oligodeoxyribonucleotides SK1 and SK2 using T4 polynucleotide kinase and T4 DNA ligase. The reaction mixture was treated with EcoRI to reconstruct the cohesive end digested with EcoRI, and the resultant EcoRI-DdeI DNA fragment (4367 bp) was ligated to the 184 bp EcoRI-DdeI DNA fragment coding Asn²⁰⁵ - Leu²⁶⁶ of the native t-PA which was obtained from the plasmid pCLiPAΔxtrp in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pMH9003 was isolated and characterized by restriction endonuclease digestion.

Example 16 (Construction and cloning of plasmid pSTTktrp)
(as illustrated in Fig. 12)

The plasmid pMH9003 was digested with StuI and the resulting DNA fragment (4551 bp) was dephosphorylated with calf intestinal phosphatase (Pharmacia AB). On the other hand, the plasmid pCLiPAΔxtrp was digested with StuI and the resultant 419bp DNA fragment coding for Gly²⁷⁹ - Ala⁴¹⁹ of the native t-PA was isolated. The resultant DNA fragment was ligated to the 4551 bp StuI DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pSTTktrp was isolated and characterized by restriction endonuclease digestion. E. coli HB101-16 was transformed with the plasmid pSTTktrp to give a transformant, E. coli HB101-16 (pSTTktrp).

Example 17 (Construction and cloning of plasmid pZY)
(as illustrated in Fig. 13)

The plasmid pTQiPAΔtrp was digested with EcoRI and StuI, and the resultant 4575 bp DNA fragment was isolated. The DNA fragment was ligated to the synthetic oligodeoxyribonucleotides HP56 and HP57 using T4 polynucleotide kinase and T4 DNA ligase. The reaction mixture was treated with EcoRI to reconstruct the cohesive end digested with EcoRI, and the resultant EcoRI-DdeI DNA fragment (4613bp) was ligated to the 184 bp EcoRI-DdeI DNA coding for Asn²⁰⁵ - Leu²⁶⁶ of the native t-PA which was prepared from the plasmid pCLiPAΔtrp in the presence of T4 DNA ligase.

The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pZY was isolated and characterized by restriction mapping.

Example 18 (Construction and cloning of plasmid pSTQitrp)
(as shown in Fig. 14)

The plasmid pZY was digested with StuI and the resulting DNA fragment (4797bp) was dephosphorylated with calf intestinal phosphatase. On the other hand, the plasmid pCLiPAΔxtrp was digested with StuI and the resultant 419 bp DNA fragment coding for Gly²⁷⁹ - Ala⁴¹⁹ of the native t-PA was isolated. The 419 DNA fragment was ligated to the 4797 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pSTQitrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with the plasmid pSTQitrp to give a transformant E. coli HB101-16 (pSTQitrp).

Example 19 (Construction and cloning of plasmid pSTQktrp)
(as illustrated in Fig. 15)

The plasmid pSTTktpr was digested with Clal and EcoRV and the resultant 4656 bp DNA fragment was isolated. On the other hand, the plasmid pSTQitrp was digested with Clal and EcoRV, and the 560 bp DNA fragment coding for Cys¹ - Asp¹⁸⁴ of STQitPA was isolated. The resulting DNA fragment was ligated to the 4656 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1.

From one of the transformants resistant to ampicillin, the desired plasmid pSTQktrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with pSTQktrp to give a transformant HB101-16 (pSTQktrp).

Example 20 (Construction and cloning of plasmid pMH9006)
(as illustrated in Fig. 16)

The plasmid pTA9004 was digested with StuI and EcoRI, and the resultant 4329 bp DNA fragment was isolated. The DNA fragment was ligated to synthetic oligodeoxyribonucleotides HP60 and HP61 using T4 polynucleotide kinase and T4 DNA ligase. The ligation mixture was digested with EcoRI to regenerate the cohesive end, digested with EcoRI, and the resultant EcoRI-DdeI DNA fragment (4364bp) was ligated to the 184 bp EcoRI-DdeI DNA fragment coding for Asn²⁰⁵ - Leu²⁵⁶ of the native t-PA which was prepared from the plasmid pCLiPAΔxtrp. The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pMH9006 was isolated and characterized by restriction mapping.

Example 21 (Construction and cloning of pthTTtrp)
(as illustrated in Fig. 17)

The plasmid pMH9006 was digested with StuI and the resultant linearized DNA fragment (4548 bp) was dephosphorylated with calf intestinal phosphatase. On the other hand, the plasmid pCLiPAΔxtrp was digested with StuI and the 419 bp DNA fragment encoding Gly²⁷⁹ - Ala⁴¹⁹ of the native t-PA was isolated. The resultant DNA fragment was ligated to the 4548 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1.

From one of the transformants resistant to ampicillin, the desired plasmid pthTTtrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with the plasmid pthTTtrp to give an transformant E. coli HB101-16 (pthTTtrp).

Example 22 (Construction and cloning of plasmid pMH9007)
(as illustrated in Fig. 18)

The plasmid pMH9003 was digested with EcoRI and EcoRV, and the 4340 bp DNA fragment was isolated. The resultant DNA fragment was ligated to the synthetic oligodeoxyribonucleotides HP58 and HP59 by using T4 polynucleotide kinase and T4 DNA ligase. The ligation mixture was treated with EcoRI to regenerate the cohesive terminal digested with EcoRI.

The resultant DNA fragment (4367 bp) was ligated to the 184 bp EcoRI-DdeI DNA fragment obtained from the plasmid pCLiPAΔxtrp in the presence of T4DNA ligase. The ligation mixture was used to transform E. coli DH-1.

From one of the transformants resistant to ampicillin, the desired plasmid pMH9007 was isolated and characterized by restriction mapping.

Example 23 (Construction and cloning of plasmid puTTtrp)
(as illustrated in Fig. 19)

The plasmid pMH9007 was digested with StuI and the resultant linearized DNA fragment (4551 bp) was dephosphorylated with calf intestinal phosphatase. On the other hand, the plasmid pCLiPAΔxtrp was digested with StuI and the resultant 419 bp DNA fragment was isolated. The 419 bp DNA fragment was ligated with the 4551 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1.

From one of the transformants resistance to ampicillin, the desired plasmid puTTtrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with the plasmid puTTtrp to give a transformant E. coli HB101-16 (puTTtrp).

Example 24 (Expression and isolation)

E. coli HB101-16 (pTQkPAΔtrp) was cultured and TQktPA was isolated from the resultant cultured broth in substantially the same manner as described in Example 9. The t-PA activity of the resultant supernatant containing TQktPA was 7.7×10^4 IU of the native t-PA/l.

Example 25 (Expression and isolation)

E. coli HB101-16 (pSTTkttrp), E. coli HB101-16(pSTQkttrp), E. coli HB101-16(pSTQittrp), E. coli HB101-16 (pthTTtrp) and E. coli HB101-16 (puTTtrp) were used for the expression of new t-PAs. Cultivation of the bacteria was carried out in substantially the same manner as that described in Example 9. The cell pellets obtained from the resultant cultured broth (200 ml) were suspended in 20 ml of 10 mM phosphate buffered saline (pH 8.0) and sonicated at 4 °C for 1 minute. After centrifugation at 15,000 rpm for 20 minutes at 4 °C, the resultant pellets were suspended in 20ml of Triton X-100 solution (0.5% Triton X-100, 8% sucrose, 50mM EDTA, 10mM Tris • HCl, pH 8.0) and sonicated at 4 °C for 1 minute. The suspension was centrifuged at 15,000 rpm for 20 minute. The resultant pellets were washed with 20 ml of 50 % aqueous glycerol and 20 ml of ice-cold ethanol, successively, and dissolved in 20 ml of 8M urea solution containing 8M urea, 20mM acetic acid, 40mM ammonium hydroxide, 0.4 mM cysteine and 0.04mM cystine, pH9.5) by sonication.

After centrifugation at 15,000 rpm for 20 minutes, the supernatant was diluted to A₂₈₀ = 0.1 (absorbance at 280nm) with the 8M urea solution. The resultant solution was dialysed against 10 times volume of aqueous solution containing 20 mM acetic acid, 40mM ammonium hydroxide, 0.4mM cysteine and 0.04mM cystine (pH 9.5) at room temperature for hours. In the above procedure, each of the dialysates containing the new t-PAs, STTktPA, STQktPA, STQitPA, thTTtPA or uTTtPA was obtained from the cultured broth of E. coli HB101-16(pSTTkttrp), E. coli HB101-16(pSTQkttrp), E. coli HB101-16(pSTQittrp), E. coli HB101-16 (pthTTtrp) or E. coli HB101-16(puTTtrp), respectively. Each of the resultant dialysates was subjected to th fibrin plate assay as described in Example 9, respectively. The results are shown in the following table.

New t-PA contained in the dialysat	Activity (IU of the native t-PA/t)
STTktPA	1.1×10^5
STQktPA	2.3×10^4
STQitPA	2.3×10^4
thTTtPA	3.7×10^4
uTTtPA	not detected *)

*)uTTtPA may be a proenzyme like pro-urokinase. Although it was inactive by fibrin plate assay, it was produced in a ratio of 29 $\mu\text{g/l}$ of the cultured broth as analysed by enzyme immunoassay.

Example 26 (Determination of molecular weights of new tPAs)

Molecular weights of the new t-PAs as produced in the above Examples were determined by SDS-PAGE analysis using marker proteins(94,000, 67,000, 45,000, 30,000, 14,400 daltons). The results are shown in the following table.

Molecular weights of the new t-PAs as produced in the above Examples were determined by SDS-PAGE analysis using marker proteins(94,000, 67,000, 45,000, 30,000, 14,400 daltons). The results are shown in the following table.

The new t-PAs	molecular weight(dalton)
TTktPA	approximately 38,000
TTitPA	approximately 38,000
TQitPA	approximately 45,000
TQktPA	approximately 45,000
STTktPA	approximately 38,000
STQktPA	approximately 45,000
STQitPA	approximately 45,000
thTTtPA	approximately 38,000
uTTtPA	approximately 38,000

Example 27 (Identification of DNA sequence)

Expression vectors were characterized and identified by restriction mapping followed by partial DNA sequencing by the dideoxyribonucleotide chain termination method [Smith, A.J.H. Meth. Enzym. 65, 560-580 (1980)] applied to double strand DNA.

The plasmid pTTkPA Δ trp (2 μg in 16 μl of 10 mM Tris \cdot HCl (pH 7.4)-1 mM EDTA) was treated with 2MM EDTA (2 μl) and 2N NaOH (2 μl) at room temperature for 5 minutes. To the resultant mixture, 5M ammonium acetate (8 μl) and EtOH (100 μl) was added. The mixture was cooled at -80°C for 30 minutes and centrifuged at 12,000 rpm for 5 minutes. After discarding the supernatant, precipitates were washed with ice-cold 70 % aqueous EtOH and dried in vacuo to give the denatured plasmid.

The plasmid was annealed with a synthetic oligodeoxyribonucleotide primer (5'-ATATTCTGAAAT-GAGCTGT, corresponding to -55--37th position of the tryptophan promoter, 5 ng) in 40 mM Tris \cdot HCl (pH 7.5)-20mM MgCl₂ -50mM NaCl at 65°C for 15 minutes followed by gently cooling to room temperature in 30 minutes. The sequencing reaction was performed with T7 polymerase (Sequenase, United States Biochemical Corp) and ^{35}S -dATP (Amersham) according to Tabor, S and Richardson, C.C.,Proc. Natl. Acad. Sci. U.S.A. 84, 4767 - 4771 (1987). The determined sequence (approximately 150 bases from the primer i.e. 35 bases in the tryptophan promoter and 115 bas s in the N-terminal coding sequence of TTktPA) was identical with that as expected.

The DNA sequence of pTQkPAA Δ trp was performed in a similar manner as described above.

The DNA sequences of pSTTkPA Δ trp, pthTT Δ trp and puTT Δ trp were performed in a similar manner as above except for using a synthetic oligodeoxyribonucleotide (5'-CTCCGGGCGACCTCCTGTG, complementary to the DNA sequence for His²⁹⁷-Gly³⁰² of native tPA).

Example 28 (Identification of amino acid sequence)

Purified STTkPA which was purified from the dialysate comprising STTkPA obtained in Example 25 by the similar purification method described in Example 12, was dissolved in 8M urea-50mM Tris⁺Hcl (pH 8.0)-1.5 % β -mercaptoethanol, and treated with monoiodoacetic acid for carboxymethylation of SH group in Cys residues. The resultant carboxymethylated STTkPA was purified by preparative HPLC using COSMOSIL 5C₄-300 (4.6 mm ϕ x 50 mm, Nakarai Tesque), and sequenced by a gas-phase sequencer 470A (Applied Biosystems Inc). The N-terminal sequence of the sample was Ser-Glu-Gly-Asn-Ser-Asp-Cys-Tyr-Phe-Gly-Asn-Gly-Ser-Ala-Tyr which was identical with the sequence as expected.

Example 29 (Construction and cloning of pST118) (as illustrated in Fig. 20)

The plasmid pST112 [an expression vector for a native t-PA which can be isolated from a transformant comprising the same, *E. coli* DH-1 FERM BP-1966, the complete cDNA sequence of a native t-PA in pST112 is illustrated in Fig. 21] was digested with *Bam*HI and *Sal*I.

The large DNA was isolated and blunted with DNA polymerase I (Klenow fragment). The resultant DNA fragment was self-ligated with T4 DNA ligase. The ligation mixture was used to transform *E. coli* HB101. From one of ampicillin resistant transformants, the objective plasmid pST118 was obtained and characterized by restriction mapping.

Example 30 (Construction and cloning of pmTQk112) (as illustrated in Fig.22 and 23)

The plasmid pST118 was digested with *Bgl*II and *Bbe*I. The large DNA fragment was isolated and ligated to synthetic *Bgl*II-*Ava*I DNAs (5'-GATCTTGCTACGAG and 5'-GTCCTCGTAGCAA, each oligomer was phosphorylated with T4 polynucleotide kinase (Takara Suzo)) coding for Arg⁻ Ser⁻ Cys³² Tyr Glu, and *Ava* II-*Bbe*I DNA coding for Asp⁹⁵ - Gly¹¹⁰ of the native tPA from pST118 with T4 DNA ligase (Takara Suzo).

The ligation mixture was used to transform *E.coli* DH-1. From one of the ampicillin resistant transformants, the objective plasmid pmTQk118 was isolated and characterized by restriction mapping.

On the other hand, the plasmid pST112 was digested with *Bgl*II and *Xma*I. The large DNA fragment was isolated and ligated to 1253 bp *Bgl*II-*Xma*I DNA coding for Arg⁻ - Val⁵⁰⁷ from pmTQk118 with T4 DNA ligase to give pmTQk112, an expression vector for mTQkPA in mammalian cell.

Example 31 (Construction and cloning of pmTTk) (as illustrated in Fig. 24, 25 and 26).

pTTkPAA Δ trp was digested with *Cla*I and *Eco*RI completely. The large DNA fragment was isolated and ligated to *Cla*I-*Dde*I synthetic DNAs (5'-CGATAAAATGGGGTCCTAGATC and 5'-TCAGATCTAGGACCCATT-TTAT, each DNA was phosphorylated with T4 polynucleotide kinase) including *Bgl*II restriction site and 91bp *Dde*I-*Eco*RI DNA coding for Glu¹⁷⁵-Trp²⁰⁴ from pTTkPAA Δ trp with T4 DNA ligase to give pHS9006. pTTkPAA Δ trp was digested with *Eco*RI (partial) and *Apa*I. The 781bp DNA fragment was isolated and ligated to 4.1 kbp *Eco*RI-*Apa*I DNA fragment from pHS9006 to give pHS3020 coding for Arg⁻ plus Ser¹⁷⁴- Pro⁵²⁷.

pHS3020 was digested with *Bgl*II and *Sma*I. The small DNA fragment coding for Arg⁻ plus Ser¹⁷⁴- Pro⁵⁰⁸ was isolated and ligated to the *Bgl*II-*Sma*I large DNA fragment from pmTQk112 to give pmTTk, an expression vector for TTkPA in mammalian cell.

Example 32 (Construction and cloning of pmSTTk)
(as illustrated in Fig.27 and 28)

pHS9006 was digested with EcoRI. The large DNA fragment was isolated, dephosphorylated with calf intestinal phosphatase (Pharmacia) and ligated to the 472bp EcoRI DNA coding for Asn²⁰⁵ - Asp²⁷⁵ - Lys³⁶¹ from pSTTkΔtrp to give pMH3025. pMH3025 was digested with BglIII and SmaI. The small DNA fragment was isolated and ligated to the large fragment BglIII-SmaI DNA from pmTQk112 to give pmSTTk, an expression vector for STTkPA in mammalian cell.

Example 33 (Expression)

Construction of L-929 Transformants

A. Preparation of the Cells

A culture of L-929 cell line was used in this example. L-929 cells can be generated from ATCC #CCL-1, and were maintained in DMEM containing kanamycin and 10% (vol/vol) fetal calf serum at 37° C in 5% CO₂. These cells were plated in a cell density of 5 x 10⁵ per 10 cm petri dish on the day before transformation, and provided 50-60% confluency on the day transformation. The media was changed three hours before the transformation. Two 10 cm petri dishes of cells were used to each transformation.

B. Preparation of the DNA solution

Plasmid DNA was introduced into L-929 cells using a calcium phosphate technique in a similar manner to that described in Gorman, DNA Cloning II, 143 (1985), IRL press.

Thirty μg of the expression plasmid (pmTQk112, pmTTk or pmSTTk) plus 3μg of plasmid pSV2neo ATCC No. 37149 was added to 186 μl of 2 M CaCl₂ and 1.3 ml of water. 1.5 ml of the DNA solution was then added dropwise to 1.5 ml of 2 x HBS (1.63% NaCl, 1.19% Hepes, 0.04% Na₂HPO₄ pH 7.12) under bubbling. The mixture was allowed to stand 30 minutes at room temperature before it was added to the cells.

C. Transfection of the cells

The 0.6 ml of the DNA solution was added to a 10 cm petri dish of L-929 cells with gentle agitation and incubated at 37° C for 18 hours in a CO₂ incubator. The cells were washed twice with DMEM. Complete fresh growth media containing 10% FCS was then added, and the cells were incubated at 37° C for 24 hours in a CO₂ incubator. The cells were trypsinized and subcultured 1:10 into selective medium composed of DMEM containing 300 μg/ml geneticin (G418) and 10% FCS.

Cells which express the phosphotransferase (neo^r gene product) can survive in the selective media and form colonies. Medium was changed every 3-4 days and colonies were isolated after 12-14 days. G418 resistant colonies were picked up by mild trypsinization in small cylinders, grown to mass cultures and tested for the secretion of mutant t-PA. The cells were grown in 1.7 cm diameter multi-well plate dishes with 3 ml of the medium to a total of about 3 x 10⁵ cells. Medium was removed and washed with PBS. Cells were cultured in 1 ml of inducible culture media composed of DMEM containing 0.04 mM ZnSO₄, 1mM sodium butyrate and 2% FCS at 37° C for 24 hours and activity of mutant t-PA in the medium was confirmed an indirect spectrophotometric assay using the chromogenic agent S2251 [Cf. Thrombosis Research 31, 427 (1983)].

E. coli DH-1 was transformed with the plasmid, pmTQk112, pmTTk or pmSTTk for the purpose of the deposit in a conventional manner.

The following microorganisms shown in the above Examples have been deposited with one of the

INTERNATIONAL DEPOSITORY AUTHORITY ON THE BUDAPEST TREATY. Fermentation Research Institute, Agency of Industrial Science and Technology residing at 1-3, Higashi 1 chome, Tsukuba-shi, Ibaraki-ken305, Japan since July 30, October 13 and November 5, 1987 and July , 1988 and were assigned the following deposit numbers, respectively.

Microorganisms	Deposit number
<u>Escherichia coli</u> HB101-16	FERM BP-1872
<u>Escherichia coli</u> HB101-16 (pTTkPA Δ trp)	FERM BP-1871
<u>Escherichia coli</u> HB101-16 (pTTiPA Δ trp)	FERM BP-1869
<u>Escherichia coli</u> HB101-16 (pTQiPA Δ trp)	FERM BP-1870
<u>Escherichia coli</u> HB101-16 (pTQkPA Δ trp)	FERM BP-1521
<u>Escherichia coli</u> HB101-16 (pSTTktrp)	FERM BP-1517
<u>Escherichia coli</u> HB101-16 (pSTQitrp)	FERM BP-1516
<u>Escherichia coli</u> HB101-16 (pSTQktrp)	FERM BP-1518
<u>Escherichia coli</u> HB101-16 (pthTTtrp)	FERM BP-1562
<u>Escherichia coli</u> HB101-16 (puTTtrp)	FERM BP-1519
<u>Escherichia coli</u> DH-1(pST112)	FERM BP-1966
<u>Escherichia coli</u> DH-1(pmTQk112)	FERM BP-1965
<u>Escherichia coli</u> DH-1(pmTTk)	FERM BP-1967
<u>Escherichia coli</u> DH-1(pmSTTk)	FERM BP-1964

Claims

1. A tissue plasminogen activator represented by the following amino acid sequence (I) as its primary structure:

180	190
R-GluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSer	
200	210
LeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysVal	
220	230
TyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArg	
240	250
AsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrp	
260	270
GluTyrCysAspValProSerCysSerThrCysGlyLeuArgGln	Y
277	280
280	290
X-GlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIle	
300	310
PheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSer	
320	330
SerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeu	
340	350
ThrValIleLeuGlyArgThrTyrArgValValProGluGluGluGluGlnLysPheGlu	
360	370
ValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAla	
380	390
LeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThr	
400	410
ValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGly	
420	430
TyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisVal	
440	450
ArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAsp	

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460 470
 AsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAla
 5 480 490
 CysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuVal
 500 510
 10 GlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLys
 520 527
 ValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro
 15 92 100
 wherein R is Ser- or CysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrp
 110 120
 20 SerThrAlaGluSerGlyAlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLys
 130 140
 ProTyrSerGlyArgArgProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCys
 25 150 160
 ArgAsnProAspArgAspSerLysProTrpCysTyrValPheLysAlaGlyLysTyrSer
 170 174
 30 SerGluPheCysSerThrProAlaCysSer-

X is -Lys-, -Ile- or bond and

Y is -TyrSerGlnProGlnPheArgIle-, -TyrSerGlnProGlnPheAspIle-, -TyrSerGlnProIleProArgSer- or -ThrLeuArgProArgPheLysIle-, and

in the above amino acid sequence, Asn¹⁸⁴, Asn²¹⁸ and Asn⁴⁴⁸ may be glycosylated.

2. The tissue plasminogen activator of claim 1, which is not glycosylated.

3. The tissue plasminogen activator of claim 1, in which R is Ser-, X is -Lys- and Y is -TyrSerGlnProGlnPheAspIle-.

4. The tissue plasminogen activator of claim 2, in which R is Ser-, X is -Lys- and Y is -TyrSerGlnProGlnPheAspIle-.

5. A DNA encoding amino acid sequence (I) as defined in claim 1.

6. A recombinant vector comprising DNA encoding amino acid sequence (I) as defined in claim 1.

7. A transformant comprising expression vector of DNA sequence encoding amino acid sequence (I) as defined in claim 1.

8. A process for the production of tissue plasminogen activator for claim 1 which comprises, culturing a host cell transformed with an expression vector comprising DNA encoding an amino acid sequence (I) as defined in claim 1 in a nutrient medium, and recovering the resultant t-PA from the cultured broth.

9. A pharmaceutical composition comprising tissue plasminogen activator of claim 1 and pharmaceutically acceptable carrier(s).

10. A finger and growth factor domains lacking tissue plasminogen activator essentially free from other proteins of human and animal origin.

11. A finger and growth factor domains lacking tissue plasminogen activator without glycosylation.

12. A tissue plasminogen activator, essentially consisting of kringle 2 domain of the heavy chain and the light chain corresponding to those of native human tissue plasminogen activator and essentially free of other proteins of human and animal origin.

13. A tissue plasminogen activator, essentially consisting of kringle 2 domain of the heavy chain and the light chain corresponding to those of native human tissue plasminogen activator without glycosylation.

14. The tissue plasminogen activator of claim 13, in which arginine residue at 275 position of the native human tissue plasminogen activator is replaced by aspartic acid residue.

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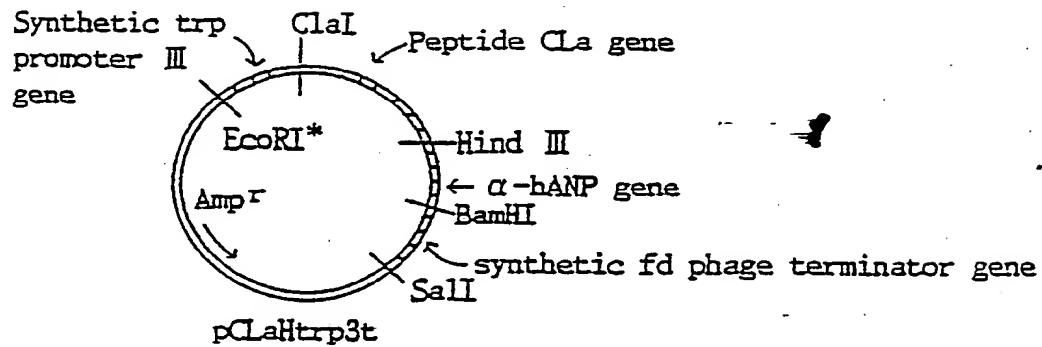
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Fig. 1 Construction and cloning of plasmid pHVBB



- digestion with BamHI and Hind III
- ligation with DNA fragment (27bp)
- transformation of E.coli DH-1 and cultivation
- isolation of plasmid pHVBB

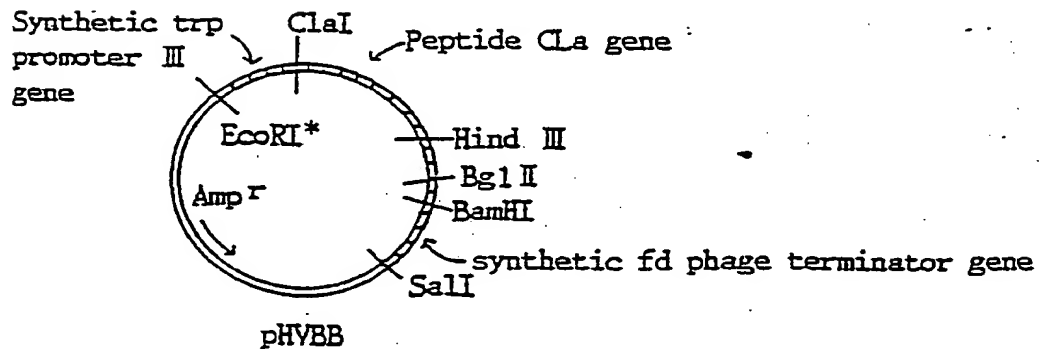


Fig. 2 Construction and cloning of plasmid pCLiPAxtrp

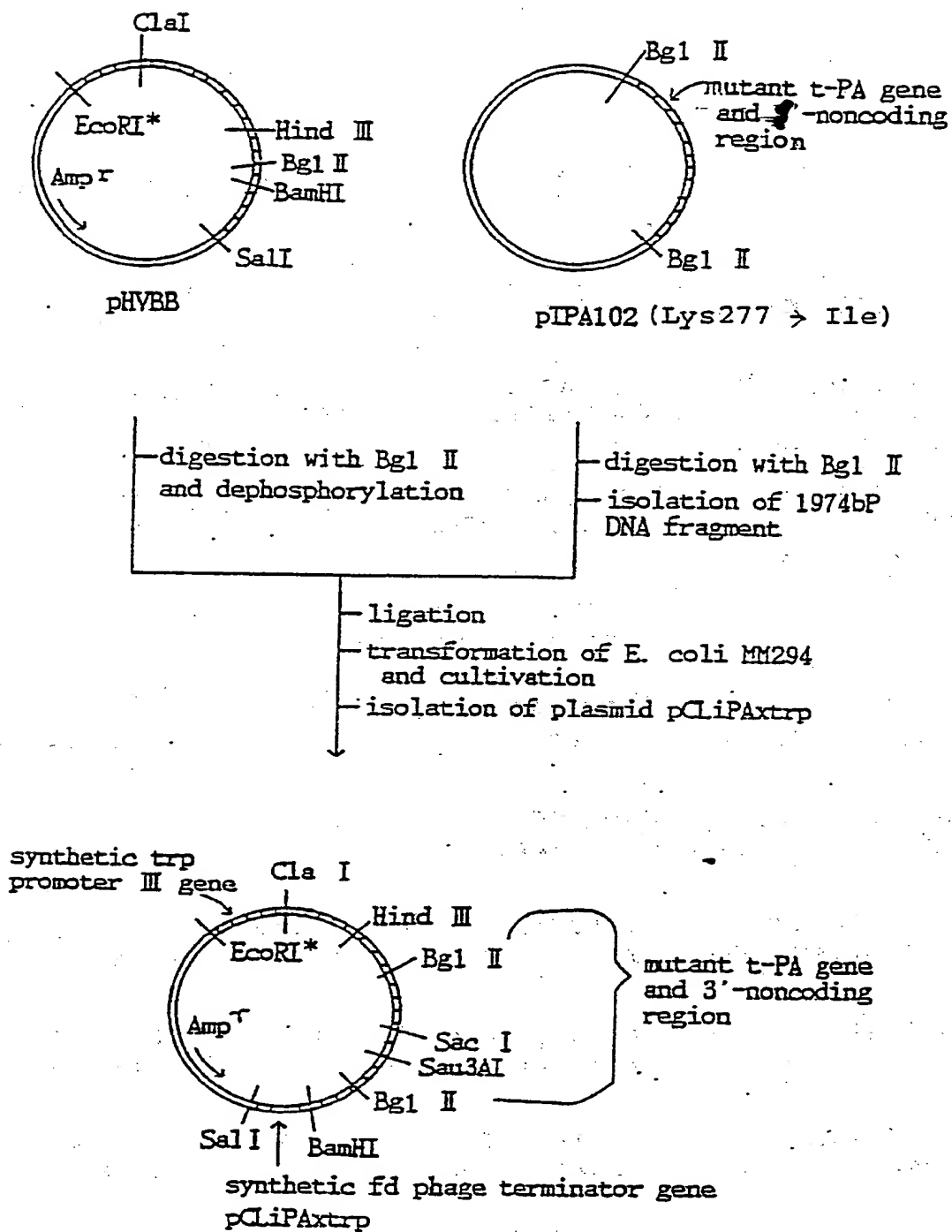


Fig.3-(1) DNA sequence of Bgl II DNA fragment(1974bp)

(Bgl II)

Coding chain: 5'-GATCTTACCAAGTGATCTGCAGAGATGAAAAACGCAGATGATATACCAG
 SerTyrGlnValIleCysArgAspGluLysThrGlnMetIleTyrGln
 ↳ Mutant t-PA 10

CAACATCAGTCAITGGCTGCGCCCTGTGCTCAGAAGCAACCGGGTGGGAATATTGCTGGTGC
 GlnHisGlnSerTrpLeuArgProValLeuArgSerAsnArgValGluTyrCysTrpCys
 20 30

AACAGTGGCAGGGCACAGTGCCACTCAGTGCCTGTCAAAGTTGCAGCGAGCCAAGGTGT
 AsnSerGlyArgAlaGlnCysHisSerValProValLysSerCysSerGluProArgCys
 40 50

TTCAACGGGGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTEGTGTGCCAGTGCCCC
 PheAsnGlyGlyThrCysGlnGlnAlaLeuTyrPheSerAspPheValCysGlnCysPro
 60 70

GAAGGATTITGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCACGTGCTACGAGGACCAG
 GluGlyPheAlaGlyLysCysCysGluIleAspThrArgAlaThrCysTyrGluAspGln
 80 90

GGCATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGCGCCGAGTGCACCAACTGG
 GlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGlyAlaGluCysThrAsnTrp
 100 110

AACAGCAGCGCGTTGGCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTG
 AsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArgProAspAlaIleArgLeu
 120 130

GGCCTGGGGAACCACAACCTACTGCAGAAACCCAGATCGAGACTCAAAGCCCTGGTGCTAC
 GlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAspSerLysProTrpCysTyr
 140 150

GTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACCCCTGCCTGCTCTGAGGGA
 ValPheLysAlaGlyLysTyrSerSerGluPheCysSerThrProAlaCysSerGluGly
 160 170

AACAGTGACTGCTACTTTGGGAATGGGTGAGCCTACCGTGGCAGGCACAGCCTCACCGAG
 AsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSerLeuThrGlu
 180 190

(EcoRI)

TCGGGTGCCTCCTGCCTCCCGTGGGAATTCCATGATCCTGATAGGCAAGGTTTACACAGCA
 SerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysValTyrThrAla
 200 210

CAGAACCCCAAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGGAATCCTGAT
 GlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnProAsp
 220 230

Fig. 3-(2)

GGGGATGCCAAGCCCTGGTGGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGT
 GlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCys
 240 250

GATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATC
 AspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArgIle
 260 270

ATAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAG
 IleGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLys
 280 290

CACAGGAGGTGCCCCGGAGAGCGGTTCTGTGCGGGGGCATACTCATCAGCTCCTGCTGG
 HisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrp
 300 310

ATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATC
 IleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIle
 320 330

TTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
 LeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLys
 340 350

(EcoRI)
 TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAG
 TyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAlaLeuLeuGln
 360 370

CTGAAATCGGATTTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCCT
 LeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCysLeu
 380 390

(SacI)
 CCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAG
 ProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGlyLys
 400 410

CATGAGGCCTTGTCTCCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTAC
 HisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeuTyr
 420 430

CCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTG
 ProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMetLeu
 440 450

TGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACCTTGCACGACGCCTGCCAGGGC
 CysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGlnGly
 460 470

GATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATC
 AspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIleIle
 480 490

Fig. 3-(3)

AGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAGGTTACCAAC
 SerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThrAsn
 500 510

TACCTAGACTGGATTTCGTGACAACATGCGACCGTGACCAGGAACACCCGACTCCTCAAAA
 TyrLeuAspTrpIleArgAspAsnMetArgPro***} → Noncoding
 520

(Sau3AI)

GCAAATGAGATCCCGCCTCTTCTTCTTCAGAAGACACTGCAAAGGCGCAGTGCTTCTCTA

CAGACTTCTCCAGACCCACCACACCGCAGAAGCGGGACGAGACCCTACAGGAGAGGGAAG

AGTGCATTTTCCCAGATACTTCCCATTTTGGAAAGTTTTCAGGACTTGGTCTGATTTTCAGG

ATACTCTGTCAGATGGGAAGACATGAATGCACACTAGCCTCTCCAGGAATGCCTCCTCCC

TGGGCAGAAAGTGGCCATGCCACCCTGTTTTGGCTAAAGGCCAACCTCCTGACCTGTCACC

GTGAGCAGCTTTGGAAACAGGACCACAAAAATGAAAGCATGTCTCAATAGTAAAAGAAAC

(Bgl II)

AAGA -3'

Fig. 4 Construction and cloning of plasmid pCLiPA Δ xtrp

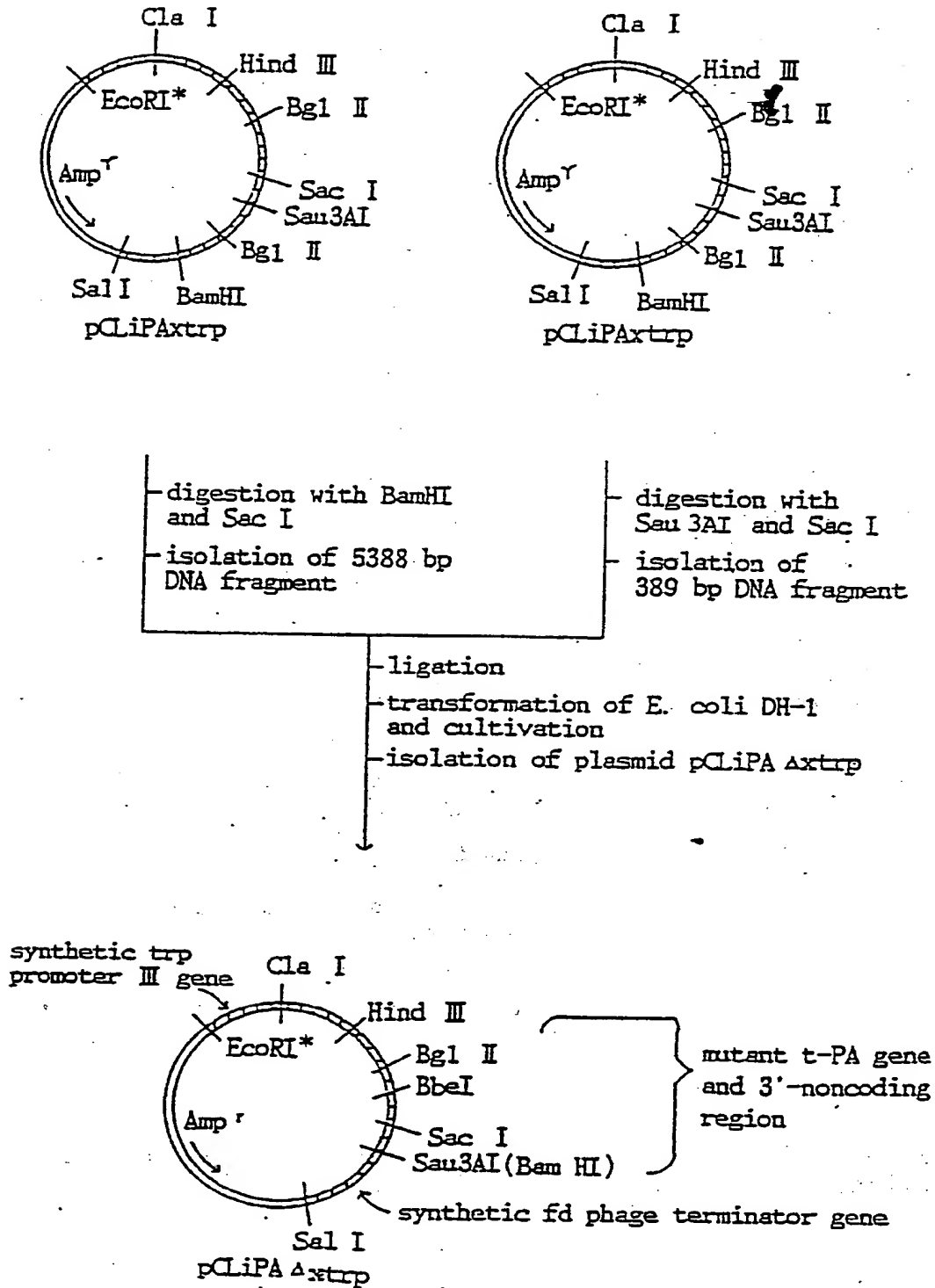


Fig. 5 Construction and cloning of plasmid pTQiPA Δ trp

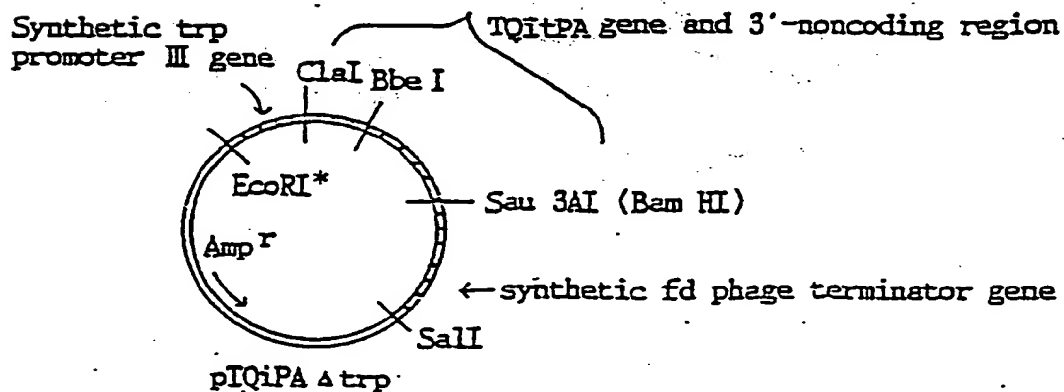
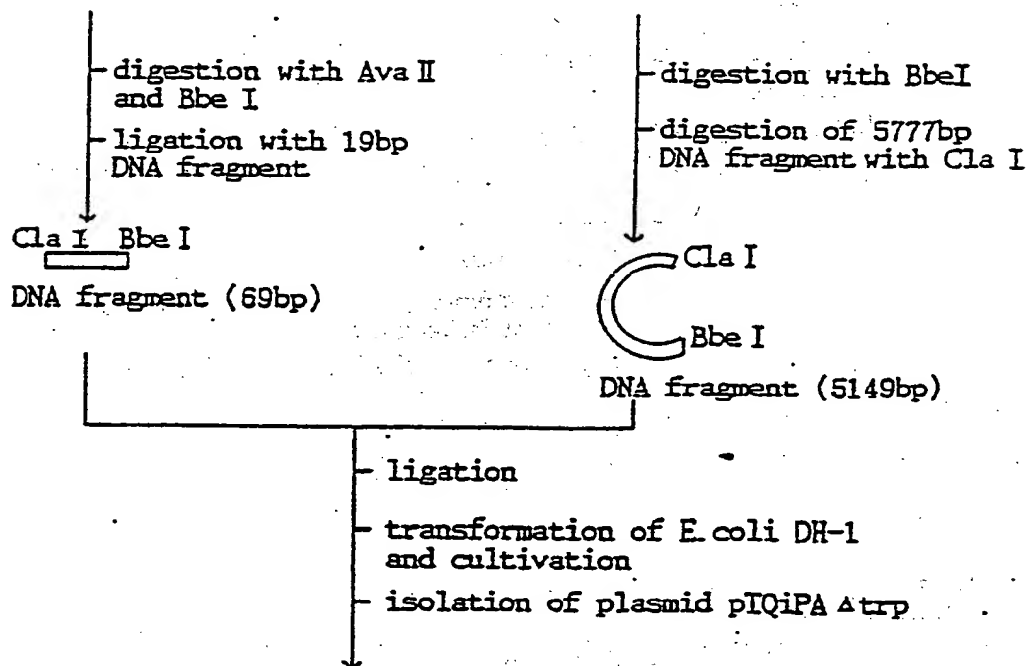
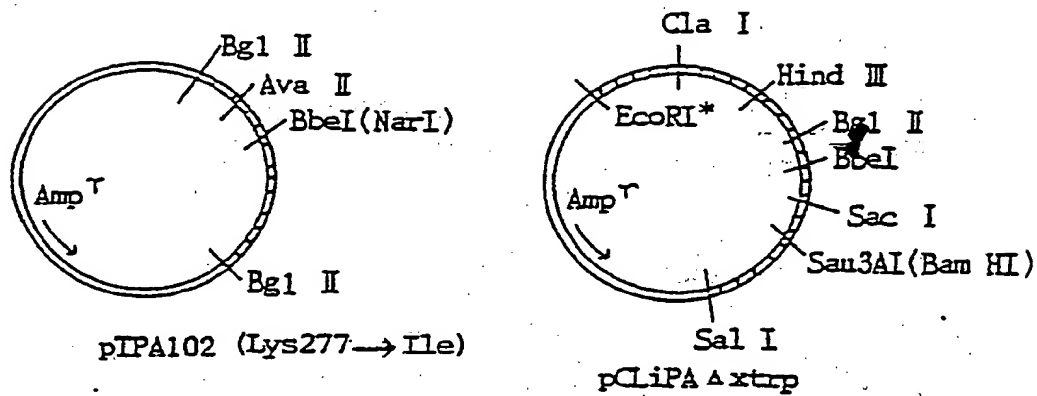


Fig. 6 Construction and cloning of plasmid pTA9004

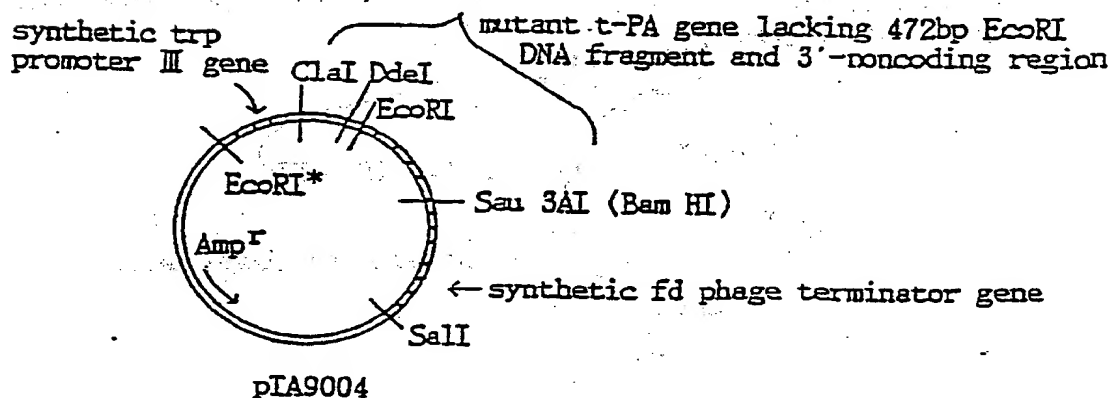
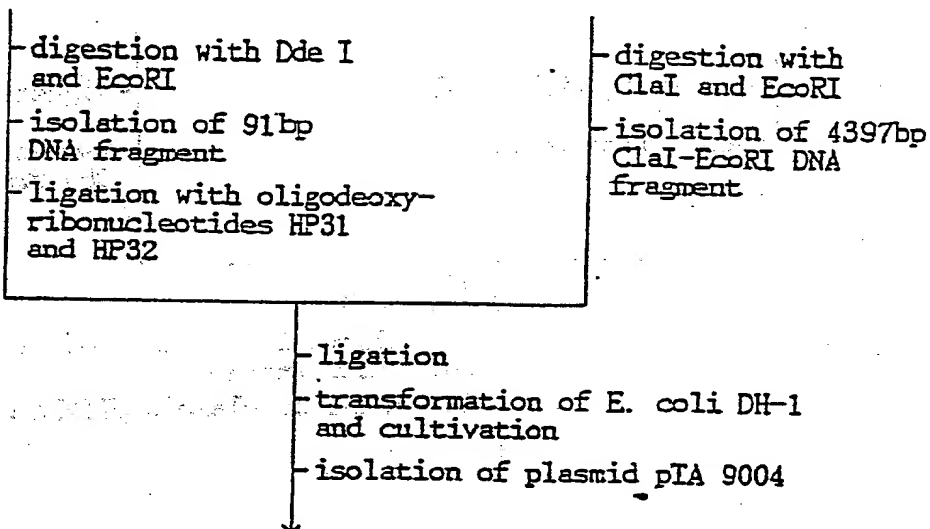
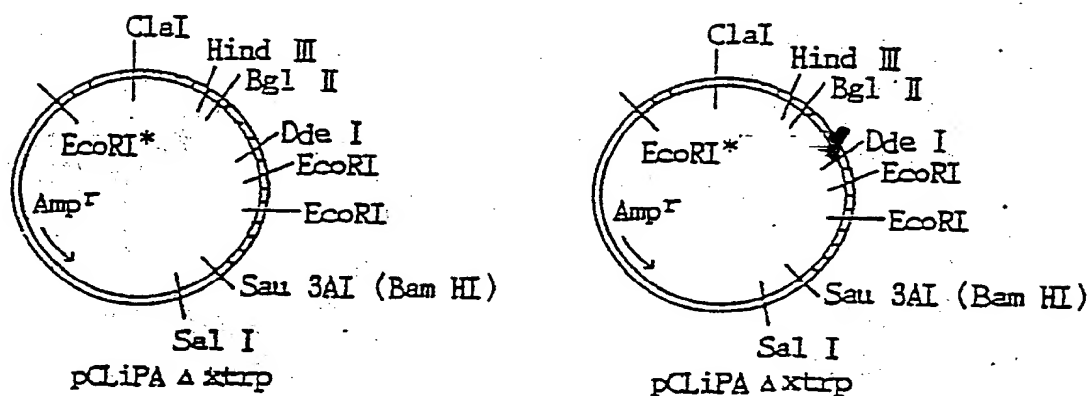


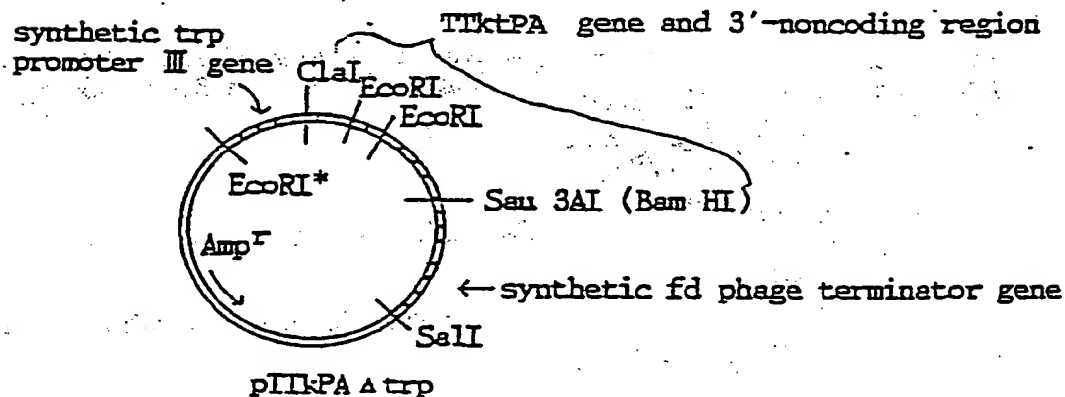
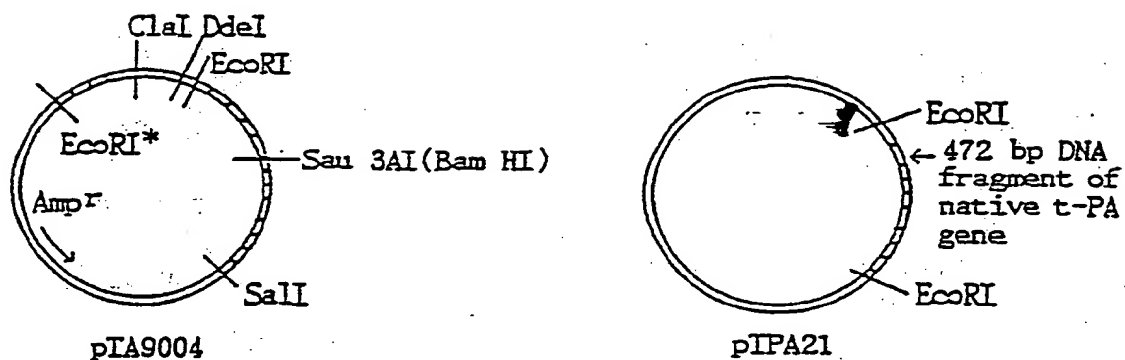
Fig. 7 Construction and cloning of plasmid pTTkPA Δ trp

Fig. 8 DNA sequence of EcoRI DNA fragment (472bp)

(EcoRI)

Coding chain: 5'-AATTCCATGATCCTGATAGGCAAGGTTTACACAGCA

Amino acid sequence: AsnSerMetIleLeuIleGlyLysValTyrThrAla

CAGAACCCCAAGTGGCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGGAATCCTGAT
GlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnProAspGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGT
GlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCysGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATC
AspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArgIleAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAG
LysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLysCACAGGAGGTGCGCCGGAGAGCGGTTCTGTGCGGGGGCATACTCATCAGCTCCTGCTGG
HisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrpATTCTCTCTGCCGCCCCTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATC
IleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIleTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
LeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLys

(EcoRI)

TACATTGTCCATAAGG -3'

TyrIleValHisLys

POOR QUALITY

Fig. 9 Construction and cloning of plasmid pTTiPAΔtrp

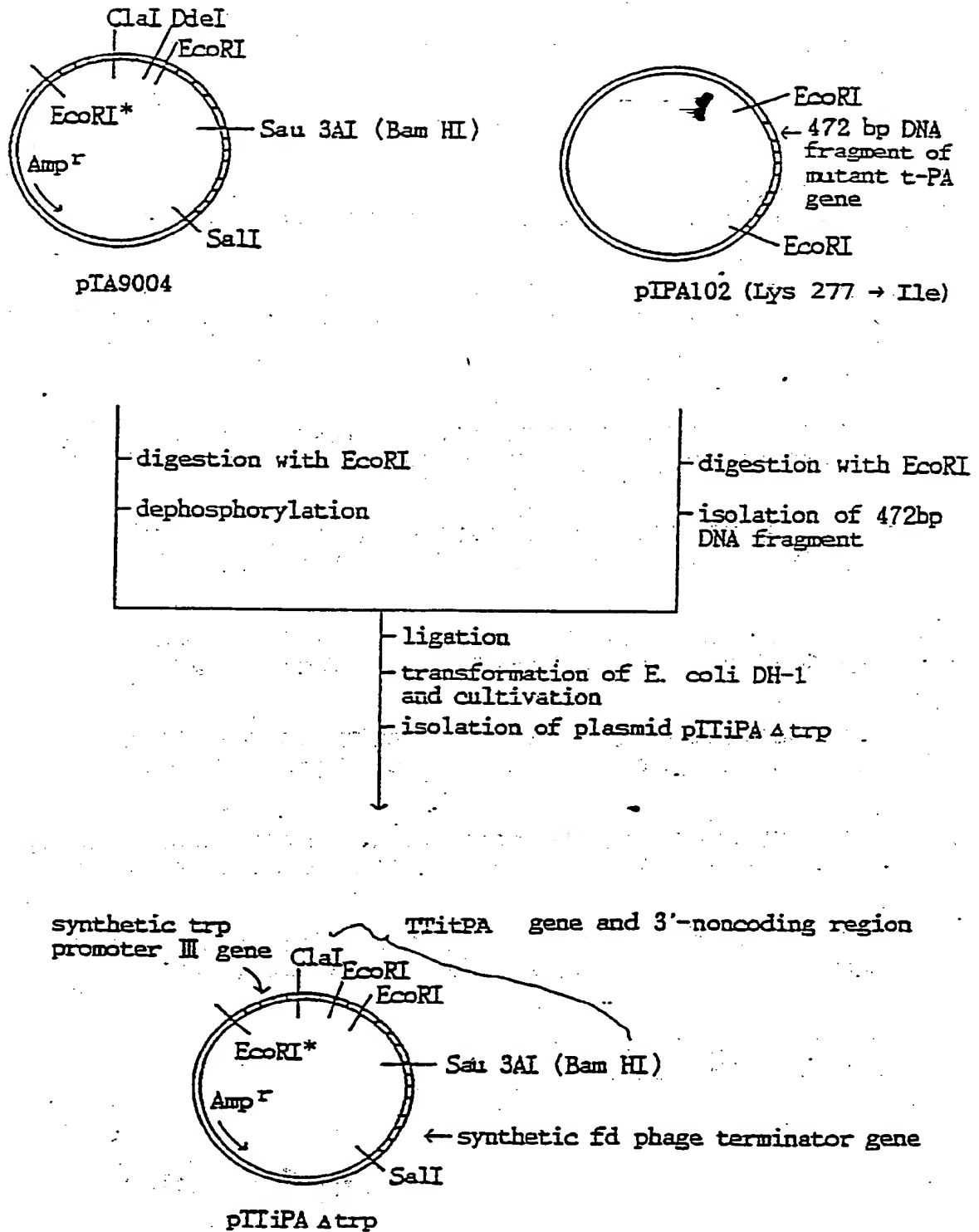


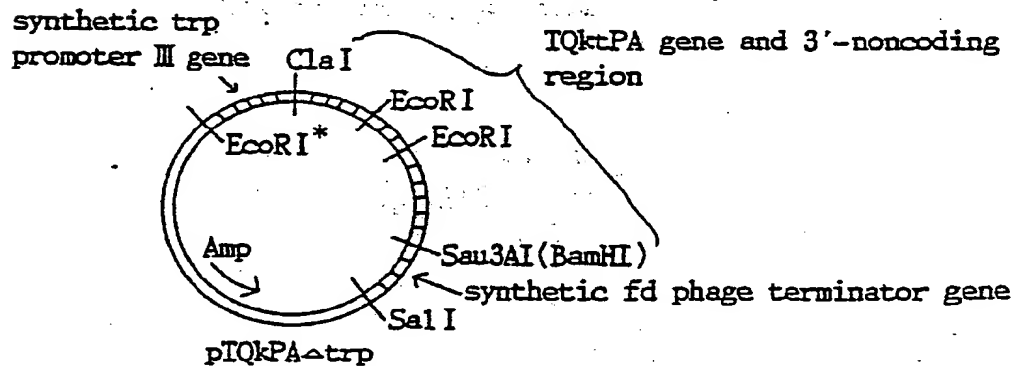
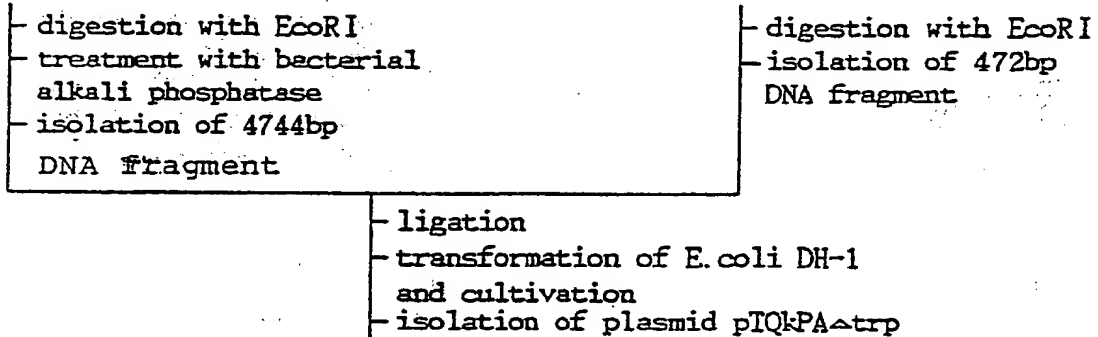
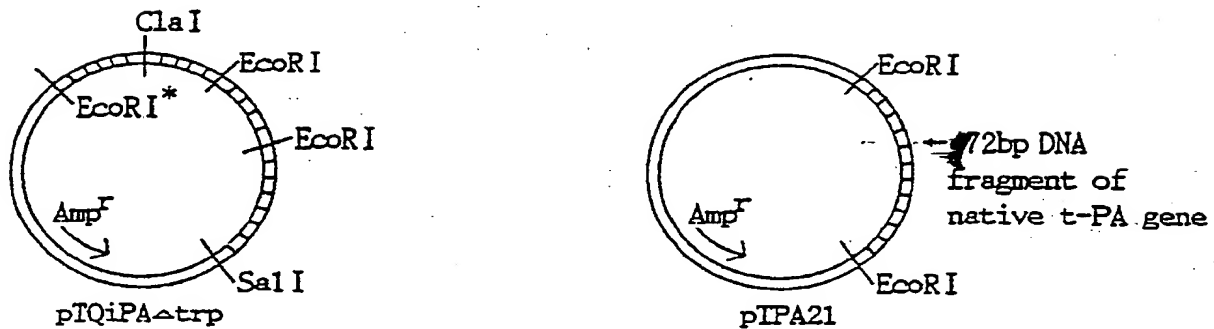
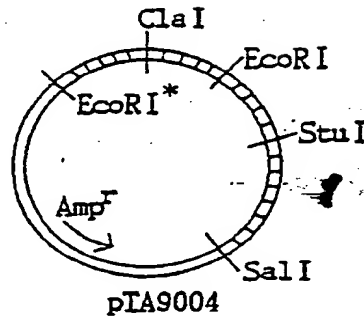
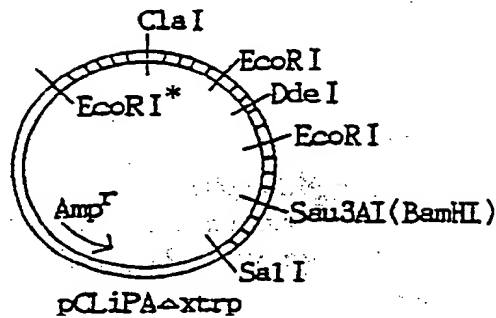
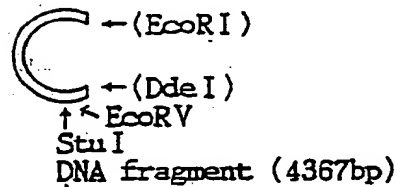
Fig.10 Construction and cloning of plasmid pTQkPA Δ trp

Fig. 11 Construction and cloning of plasmid pMH9003



digestion with EcoRI
 and DdeI
 isolation of 184 bp
 DNA fragment
 ↓
 (EcoRI) (DdeI)
 DNA fragment (184bp)

digestion with EcoRI and
 StuI
 isolation of 4329 bp DNA
 fragment
 ligation with synthetic
 oligodeoxyribonucleotides
 SK1 and SK2
 treatment with EcoRI
 isolation of 4367 bp
 DNA fragment
 ↓



ligation
 transformation of E.coli DH-1 and
 cultivation
 isolation of plasmid pMH9003
 ↓

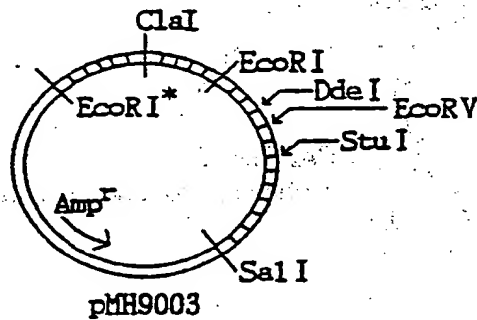
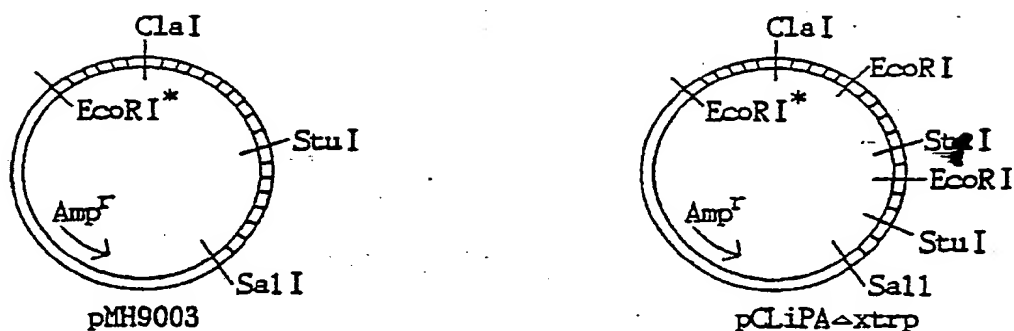


Fig. 12 Construction and cloning of plasmid pSTItktrp



- digestion with StuI
 - isolation of 4551bp
 DNA fragment
 - treatment with calf
 intestinal phosphatase

- digestion with StuI
 - isolation of 419bp
 DNA fragment

- ligation
 - transformation of E. coli DH-1
 and cultivation
 - isolation of plasmid pSTItktrp

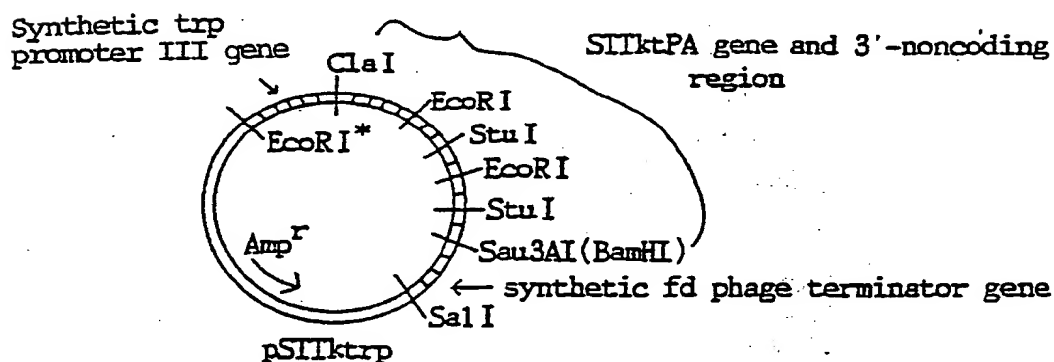


Fig.13 Construction and cloning of plasmid pZY

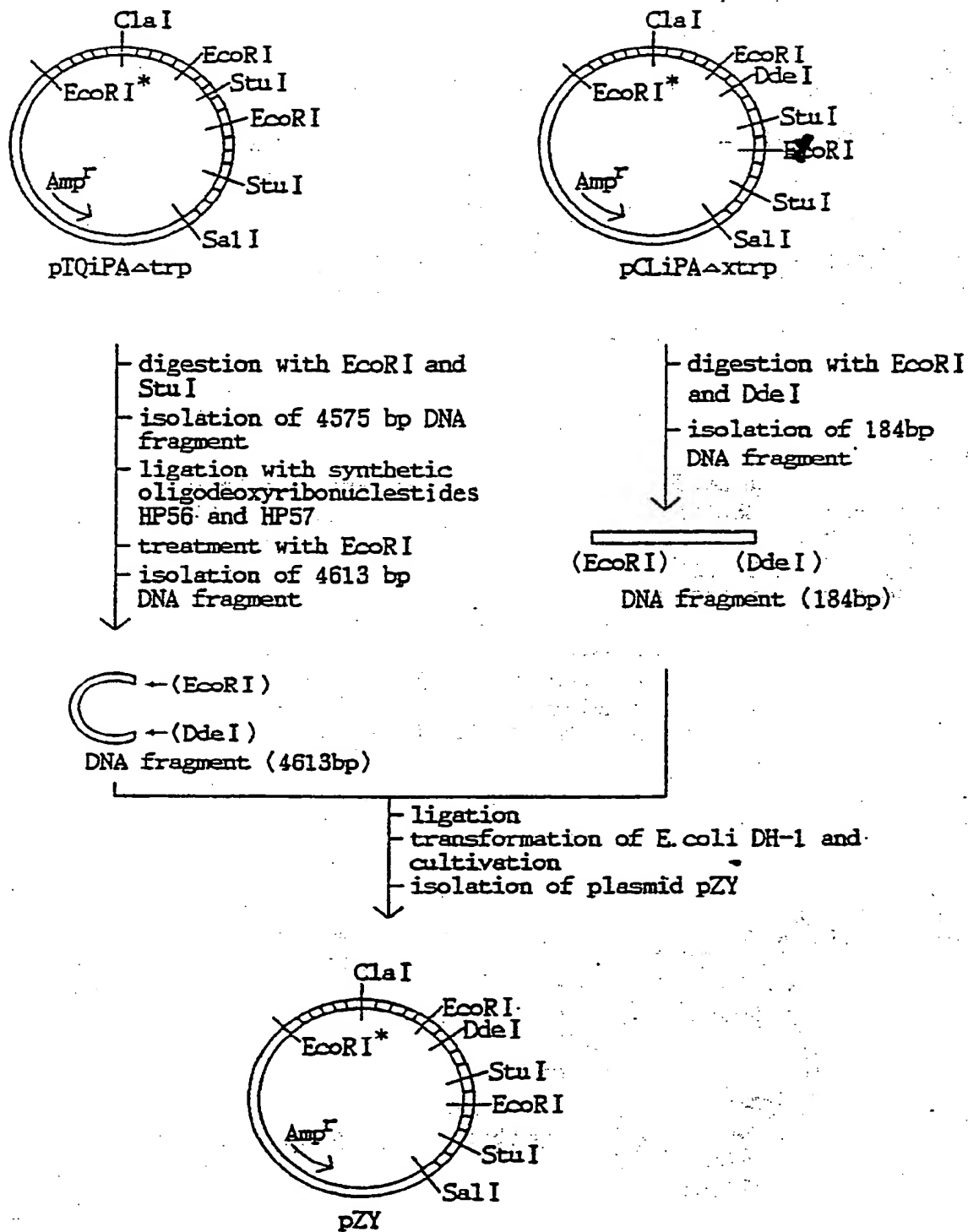


Fig. 14 Construction and cloning of plasmid pSTQitrp

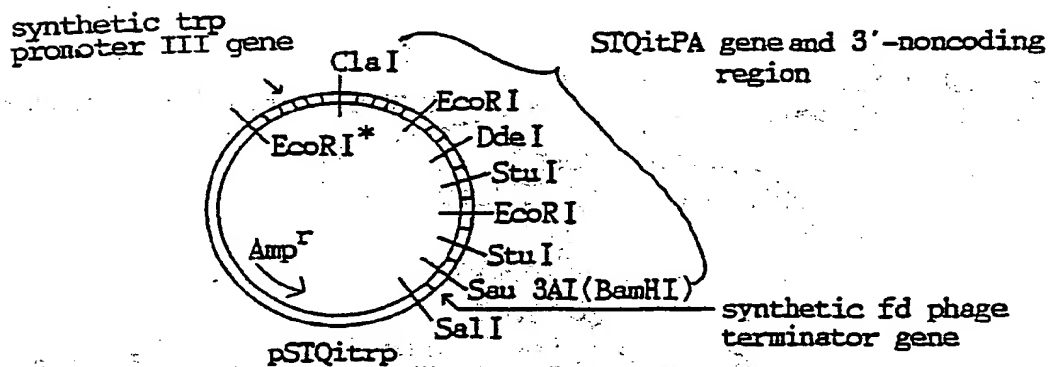
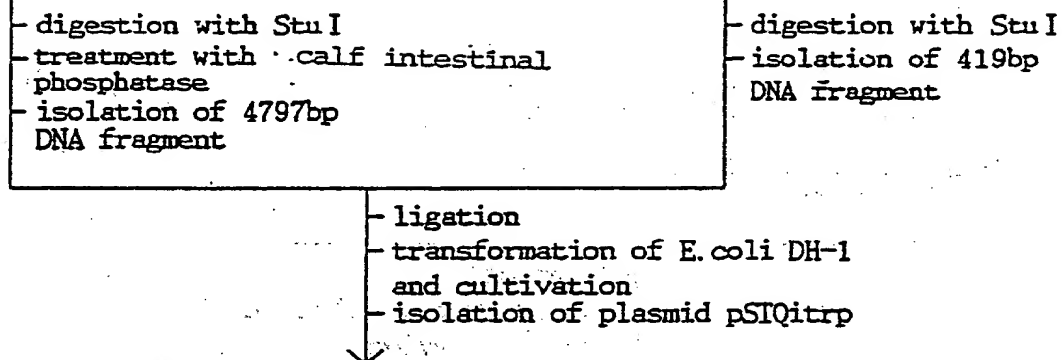
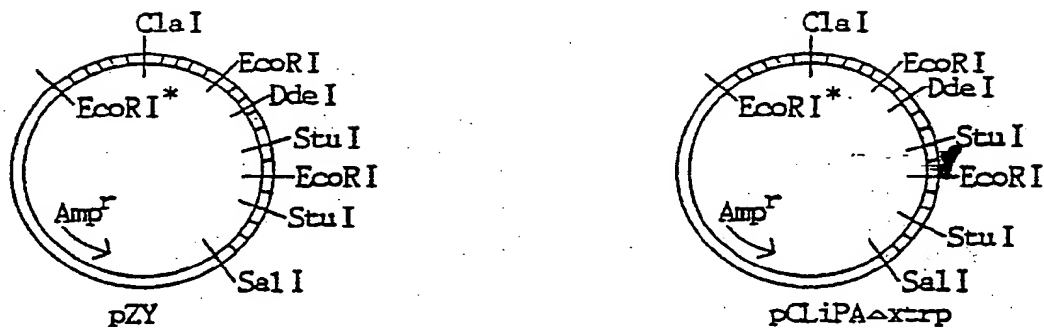


Fig. 15 Construction and cloning of plasmid pSTQktrp

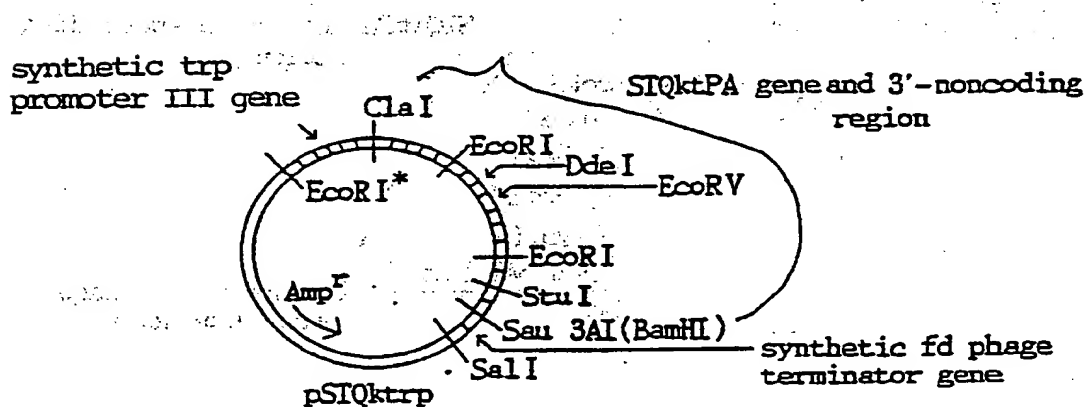
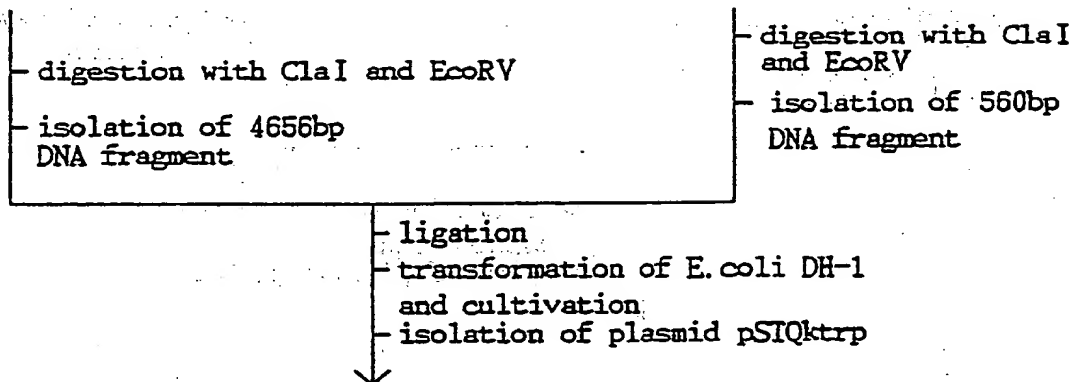
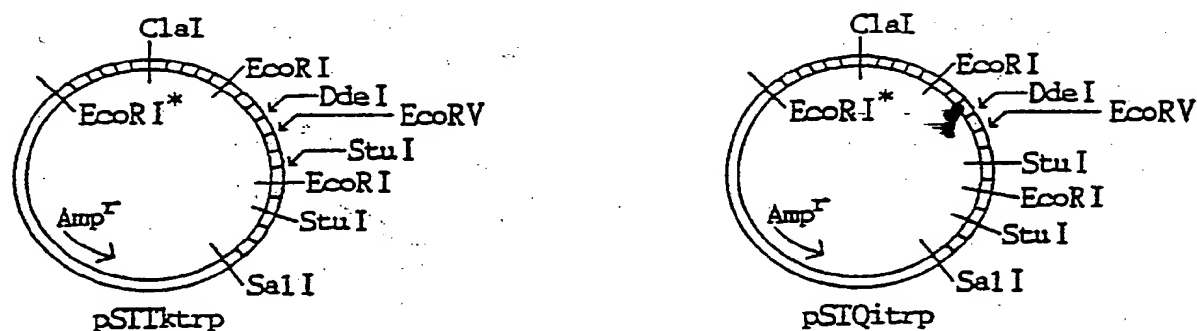


Fig. 16 Construction and cloning of plasmid pMH9006

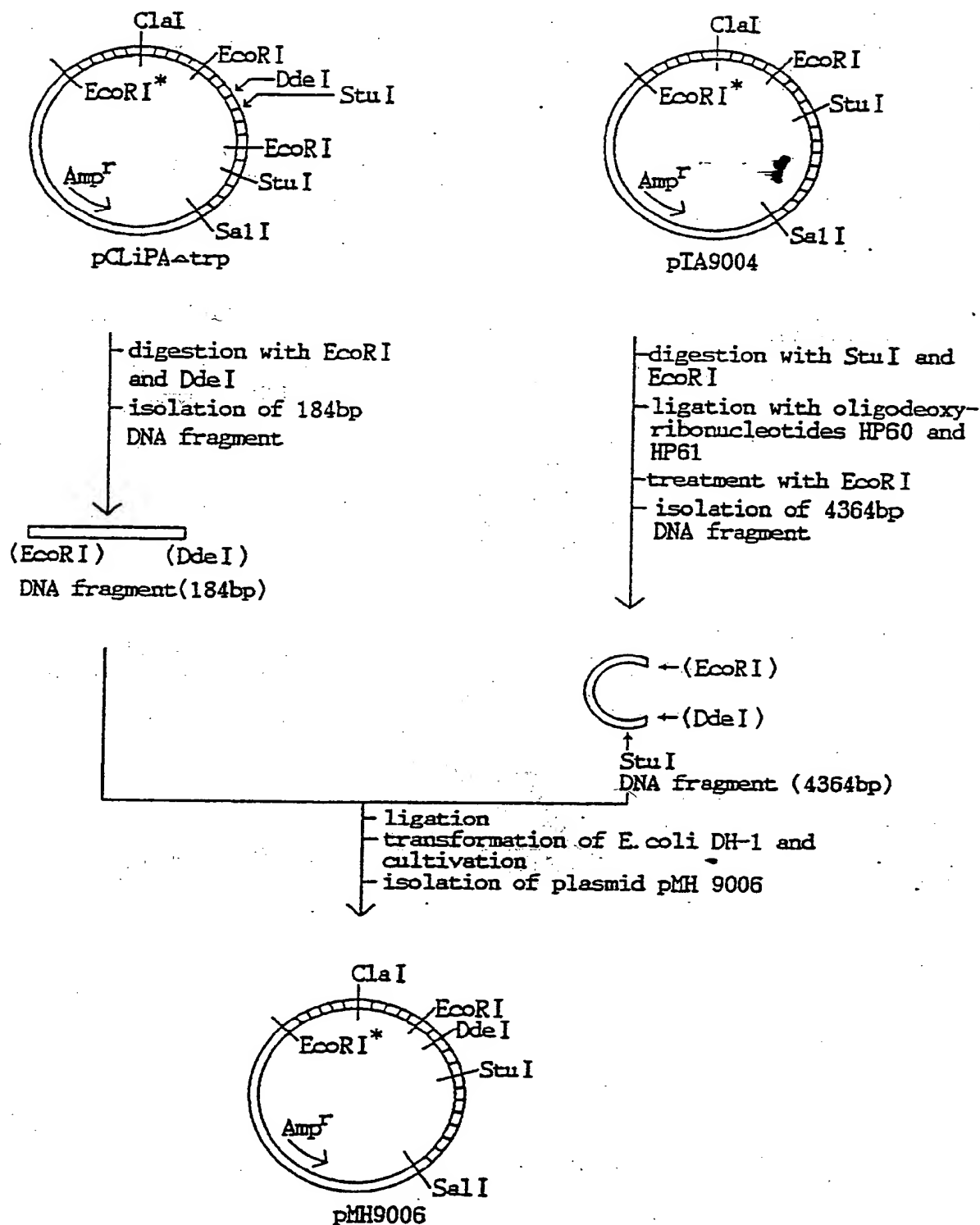


Fig. 17 Construction and cloning of plasmid pthIIItrp

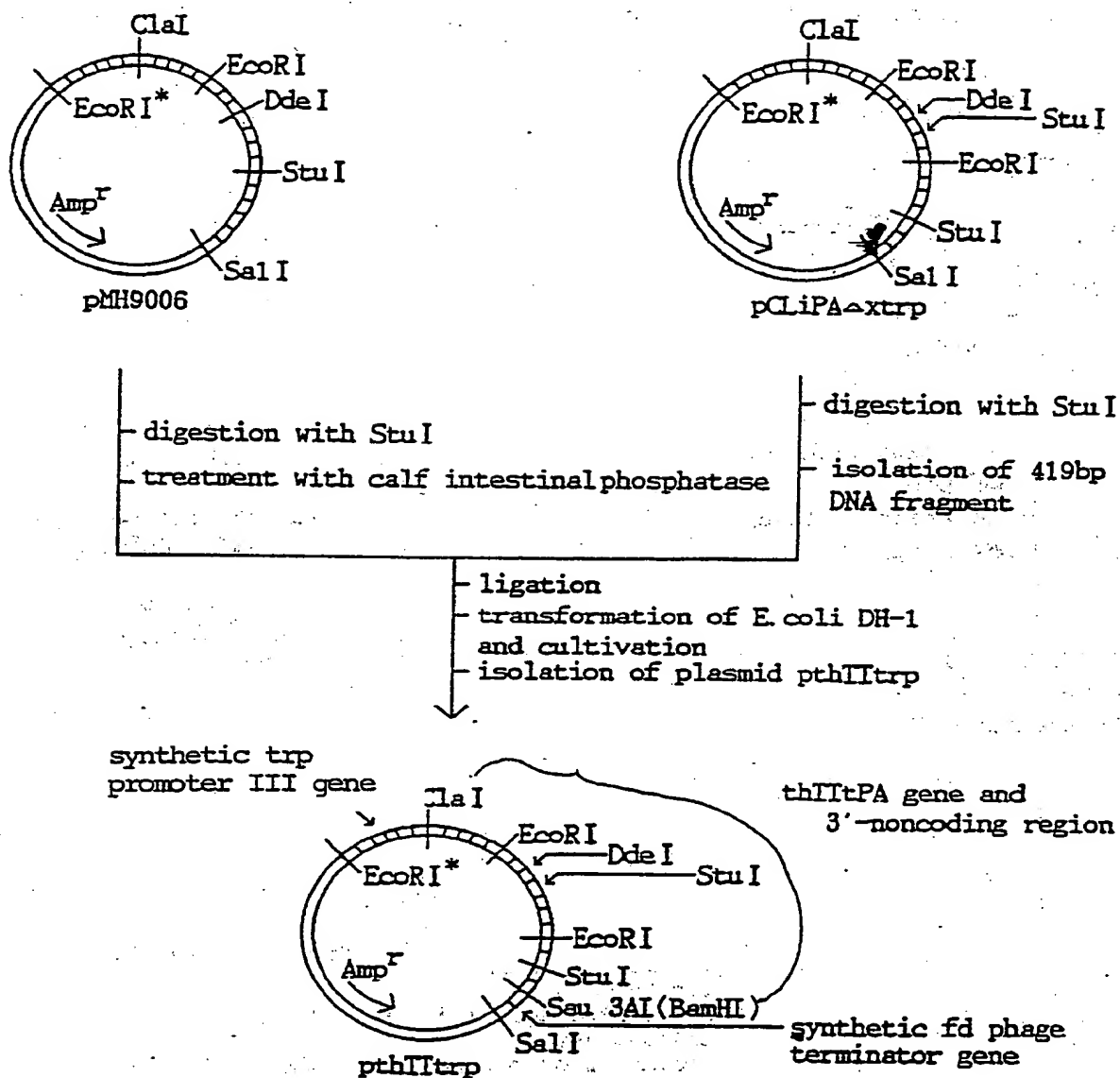


Fig.18 Construction and cloning of plasmid pMH9007

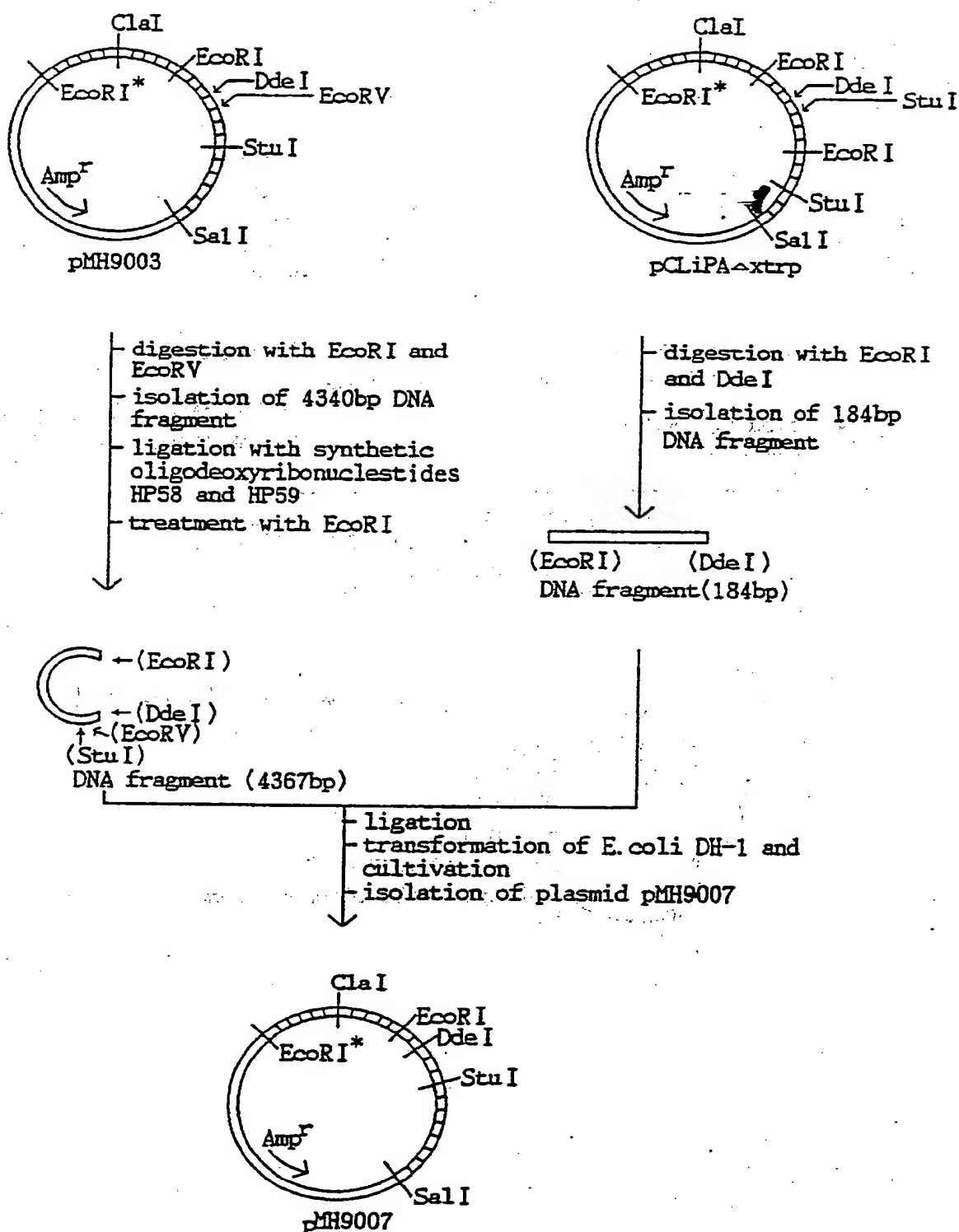


Fig. 19 Construction and cloning of plasmid puITtrp

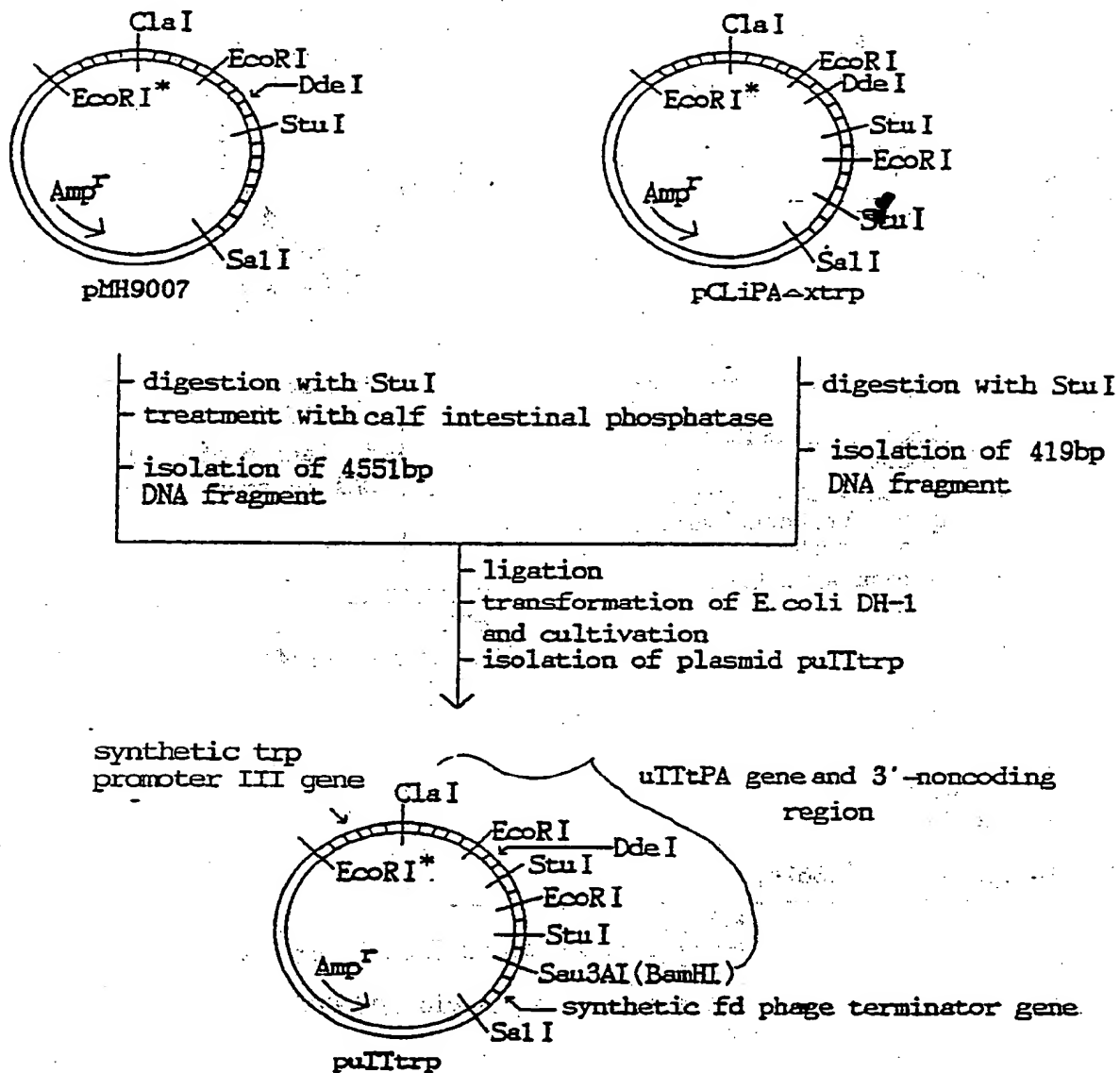


Fig. 20. Construction and cloning of plasmid pST118

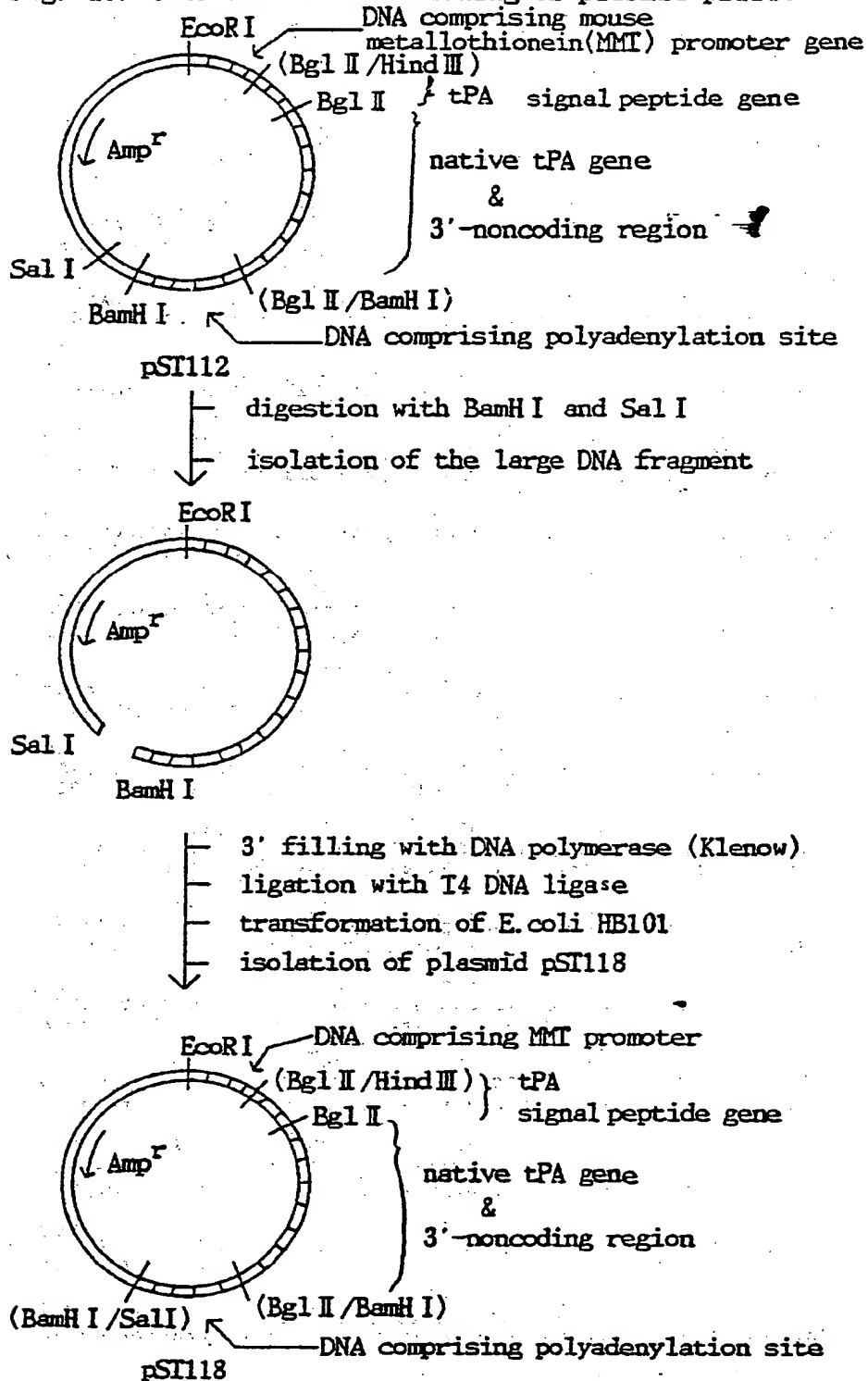


Fig. 21-(1). cDNA sequence of a native tPA in PST112
 (Upper: Coding chain
 Lower: Coded amino acid sequence)

```

5' - GTTAAGGGACGCTGTGAAGCAATCATGGATGCAATGAAGAGAGGGGCTCTGCTGTGTGCTG
      10      20      30      40      50      60
      MetAspAlaMetLysArgGlyLeuCysCysValLeu

      70      80      90      100     110     120
CTGCTGTGTGGAGCAGTCTTCGTTTCGCCAGCCAGGAAATCCATGCCCGATCAGAAGA
LeuLeuCysGlyAlaValPheValSerProSerGlnGluIleHisAlaArgPheArgArg

      130     140     150     160     170     180
GGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAXAAAACGCAGATGATATACCAGCAA
GlyAlaArgSerTyrGlnValIleCysArgAspGluLysThrGlnMetIleTyrGlnGln
      190 native tPA 200     210     220     230     240
CATCAGTCATGGCTGCGCCCTGTGCTCAGAAGCAACCGGGTGAATATTGCTGGTGCAAC
HisGlnSerTrpLeuArgProValLeuArgSerAsnArgValGluTyrCysTrpCysAsn

      250     260     270     280     290     300
AGTGGCAGGGCACAGTGCCACTCAGTGCCTGTCAAAAGTTGCAGCGAGCCAAGGTGTTTC
SerGlyArgAlaGlnCysHisSerValProValLysSerCysSerGluProArgCysPhe

      310     320     330     340     350     360
AACGGGGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTCTGTGCCAGTGCCCCGAA
AsnGlyGlyThrCysGlnGlnAlaLeuTyrPheSerAspPheValCysGlnCysProGlu

      370     380     390     400     410     420
GGATTTGCTGGGAAGTGCTGTGAAATAGATACAGGGCCACGTGCTACGAGGACCAGGGC
GlyPheAlaGlyLysCysCysGluIleAspThrArgAlaThrCysTyrGluAspGlnGly

      430     440     450     460     470     480
ATCAGTACAGGGGCACGTGGAGCACAGCGAGAGTGGCGCCGAGTGCCACCAACTGGAAC
IleSerTyrArgGlyThrTrpSerThrAlaGluSerGlyAlaGluCysThrAsnTrpAsn

      490     500     510     520     530     540
AGCAGCGCGTTGGCCCAGAACCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGGGC
SerSerAlaLeuAlaGlnLysProTyrSerGlyArgArgProAspAlaIleArgLeuGly

      550     560     570     580     590     600
CTGGGGAACCACTACTGCAGAAACCCAGATCGAGACTCAAAGCCCTGGTGCTACGTC
LeuGlyAsnHisAsnTyrCysArgAsnProAspArgAspSerLysProTrpCysTyrVal

      610     620     630     640     650     660
TTTAAGGCGGGAAGTACAGCTCAGAGTTCTGCAGCACCCCTGCCTGCTCTGAGGGAAC
PheLysAlaGlyLysTyrSerSerGluPheCysSerThrProAlaCysSerGluGlyAsn

      670     680     690     700     710     720
AGTGACTGCTACTTTGGGAATGGGTGAGCCTACCGTGGCACGCACAGCCTCACCAGTCTG
SerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSerLeuThrGluSer

      730     740     750     760     770     780
GGTGCCCTCCTGCCTCCCGTGGAAATCCATGATCCTGATAGGCAAGGTTTACACAGCACAG
GlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysValTyrThrAlaGln

      790     800     810     820     830     840
AACCCCACTGCCAGGCAGTGGGCTGGGCAAACATAATTACTGCCGGAATCCTGATGGG
AsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnProAspGly

      850     860     870     880     890     900
GATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGAT
AspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCysAsp

      910     920     930     940     950     960
GTGCCCTCCTGCTCCACCTGCGGCTGAGACAGTACAGCCAGCCTCAGTTTCGATCAAA
ValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArgIleLys

      970     980     990     1000    1010    1020
GGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAGCAC
GlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLysHis

      1030    1040    1050    1060    1070    1080
AGGAGGTGCGCCCGGAGAGCGGTTCTGTGCGGGGCATACTCATCAGCTCCTGCTGGATT
ArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrpIle

```

Fig. 21-(2).

1090 1100 1110 1120 1130 1140
 CTCTCTGCCGCCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTG
 LeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIleLeu
 1150 1160 1170 1180 1190 1200
 GGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATAC
 GlyArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLysTyr
 1210 1220 1230 1240 1250 1260
 ATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAGCTG
 IleValHisLysGluPheAspAspThrTyrAspAsnAspIleAlaLeuLeuGlnLeu
 1270 1280 1290 1300 1310 1320
 AAATCGGATTTCGTCCTGTCGCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTTCCC
 LysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCysLeuPro
 1330 1340 1350 1360 1370 1380
 CCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCAT
 ProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGlyLysHis
 1390 1400 1410 1420 1430 1440
 GAGGCCTTGTCTCCTTTCTATTCCGAGCGGCTGAAGGAGGCTCATGTGCACTGTACCCA
 GluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeuTyrPro
 1450 1460 1470 1480 1490 1500
 TCCAGCCGCTGCACATCACAACTTTACTTAACAGAACAGTCACCGACAACATGCTGTGT
 SerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMetLeuCys
 1510 1520 1530 1540 1550 1560
 GCTGGAGACACTCGGAGCGGGCGGGCCCCAGGCAAACTTGCACGACGCTGCCAGGGCGAT
 AlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGlnGlyAsp
 1570 1580 1590 1600 1610 1620
 TCGGGAGGGCCCCCTGGTGTGTCTGAACGATGGCCGCTGACTTTGGTGGGCATCATCAGC
 SerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIleIleSer
 1630 1640 1650 1660 1670 1680
 TGGGGCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAGGTTACCAACTAC
 TrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThrAsnTyr
 1690 1700 1710 1720 1730 1740
 CTAGACTGGATTTCGTGACAACATGCCACCGTGACCAGGAACACCCGACTCCTCAAAAGCA
 LeuAspTrpIleArgAspAsnMetArgPro***
 1750 1760 1770 1780 1790 1800
 AATGAGATCCCGCCTCTTCTTTCAGAAGACACTGCAAAGGCGCAGTGCTTCTCTACAG
 1810 1820 1830 1840 1850 1860
 ACTTCTCCAGACCCACCACACCGCAGAAGCGGGACGAGACCTACAGGAGAGGGAAGAGT
 1870 1880 1890 1900 1910 1920
 GCATTTTCCAGATACTTCCATTTTGAAGTTTTTCAGGACTTGGTCTGATTTTCAGGATA
 1930 1940 1950 1960 1970 1980
 CTCTGTGATGGGAAGACATGAATGCACACTAGCCTCTCCAGGAATGCTCCTCCTG
 1990 2000 2010 2020 2030 2040
 GCAGAAGTGGCCATGCCACCCTGTTTTTCGCTAAAGCCCAACCTCCTGACCTGTCACCGTG
 2050 2060 2070 2080 2090 2100
 AGCAGCTTTGGAACAGGACCACAAAAATGAAAGCATGTCTCAATAGTAAAGAAACAAG

Fig. 22. Construction and cloning of plasmid pmTQk118

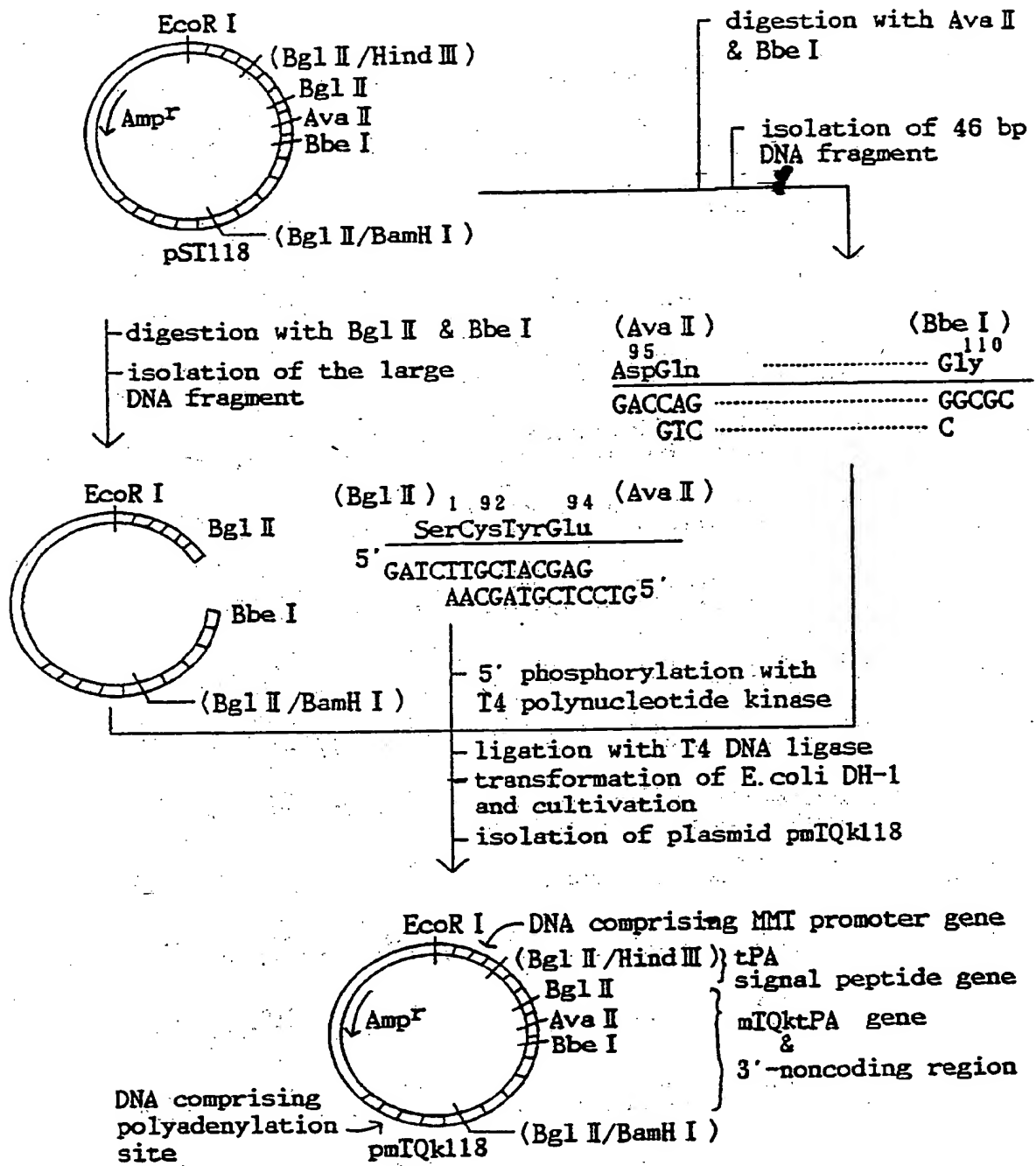


Fig. 23. Construction and cloning of plasmid pmTQk112

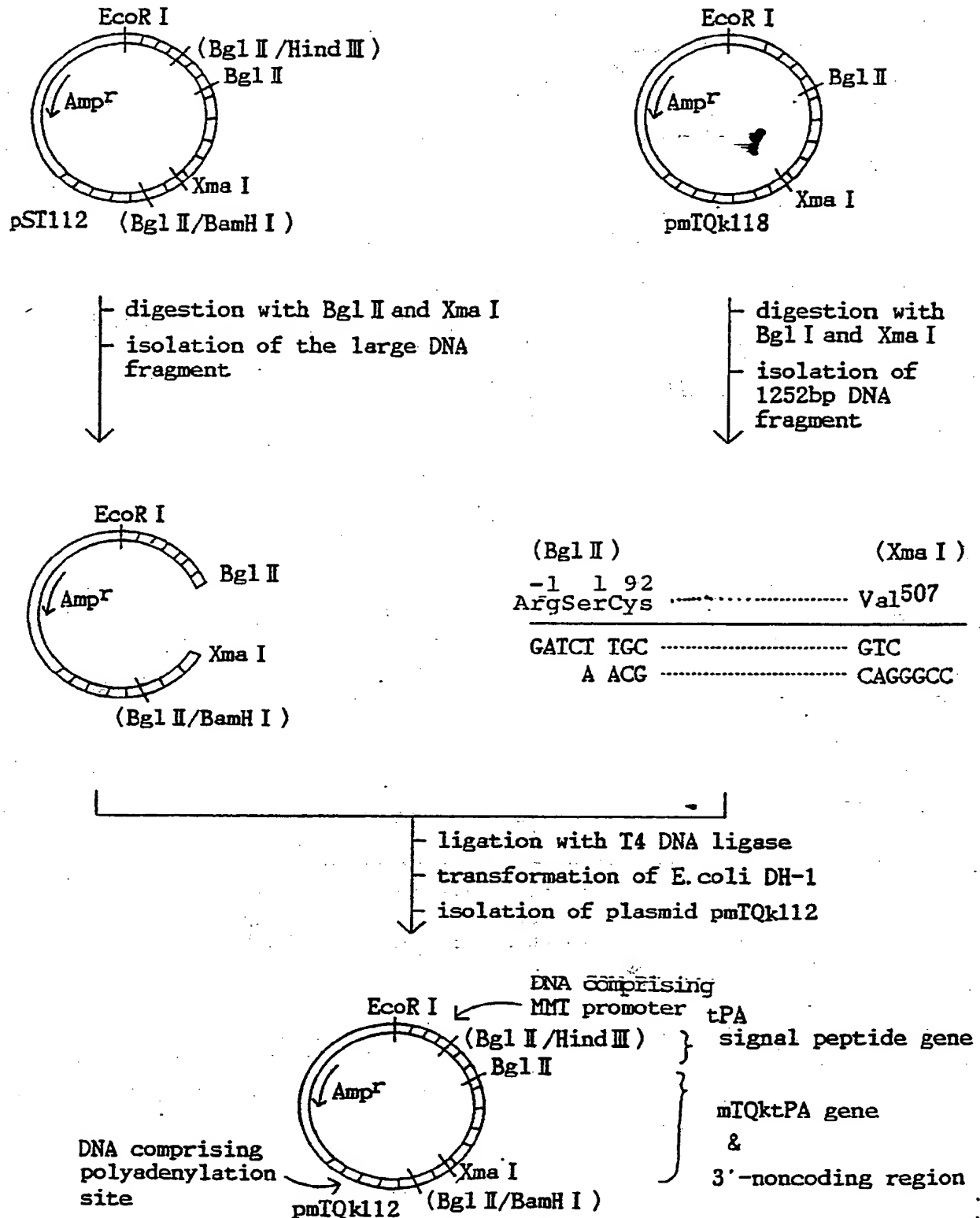


Fig. 24. Construction and cloning of plasmid pHS9006

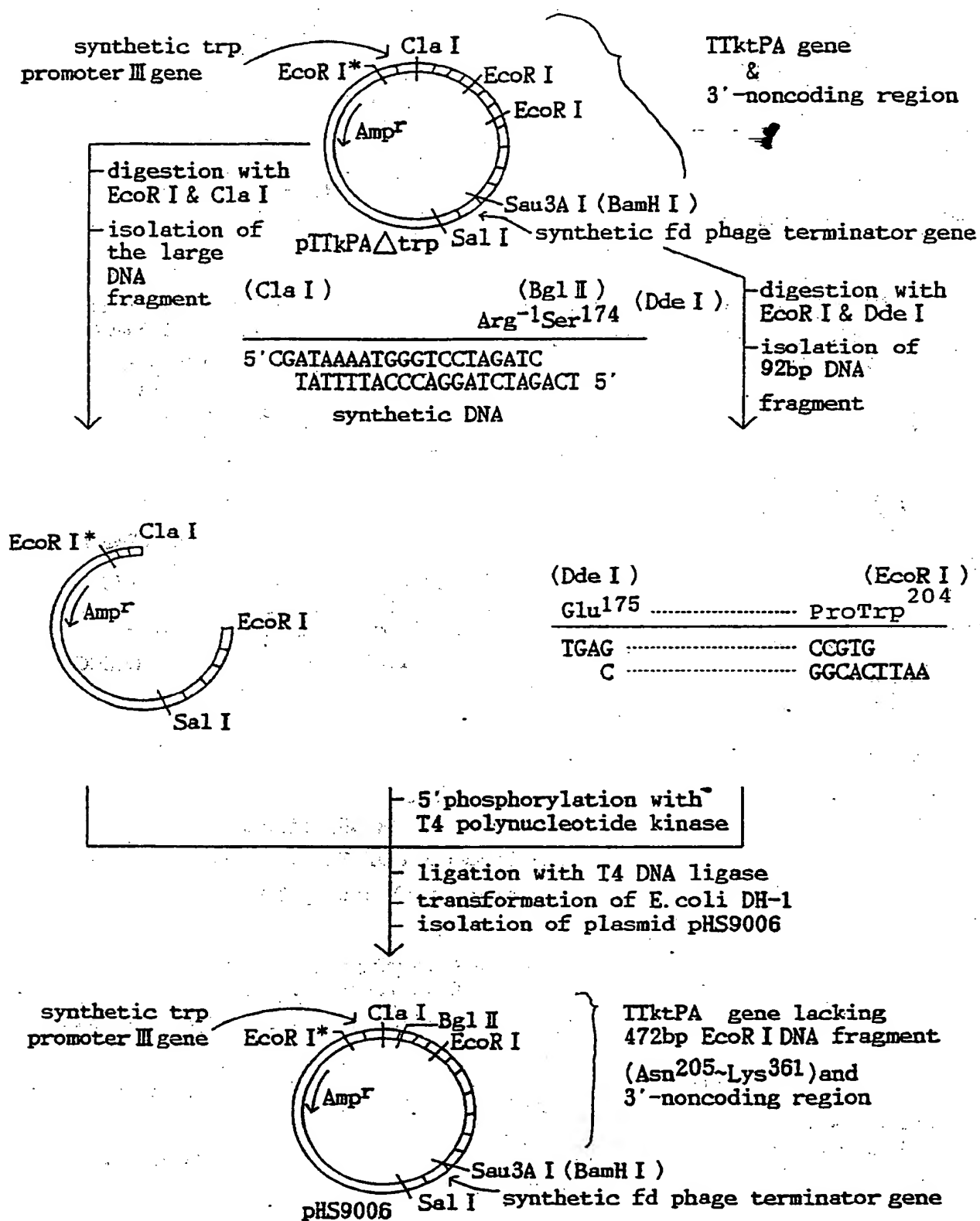


Fig. 25. Construction and cloning of plasmid pHS3020

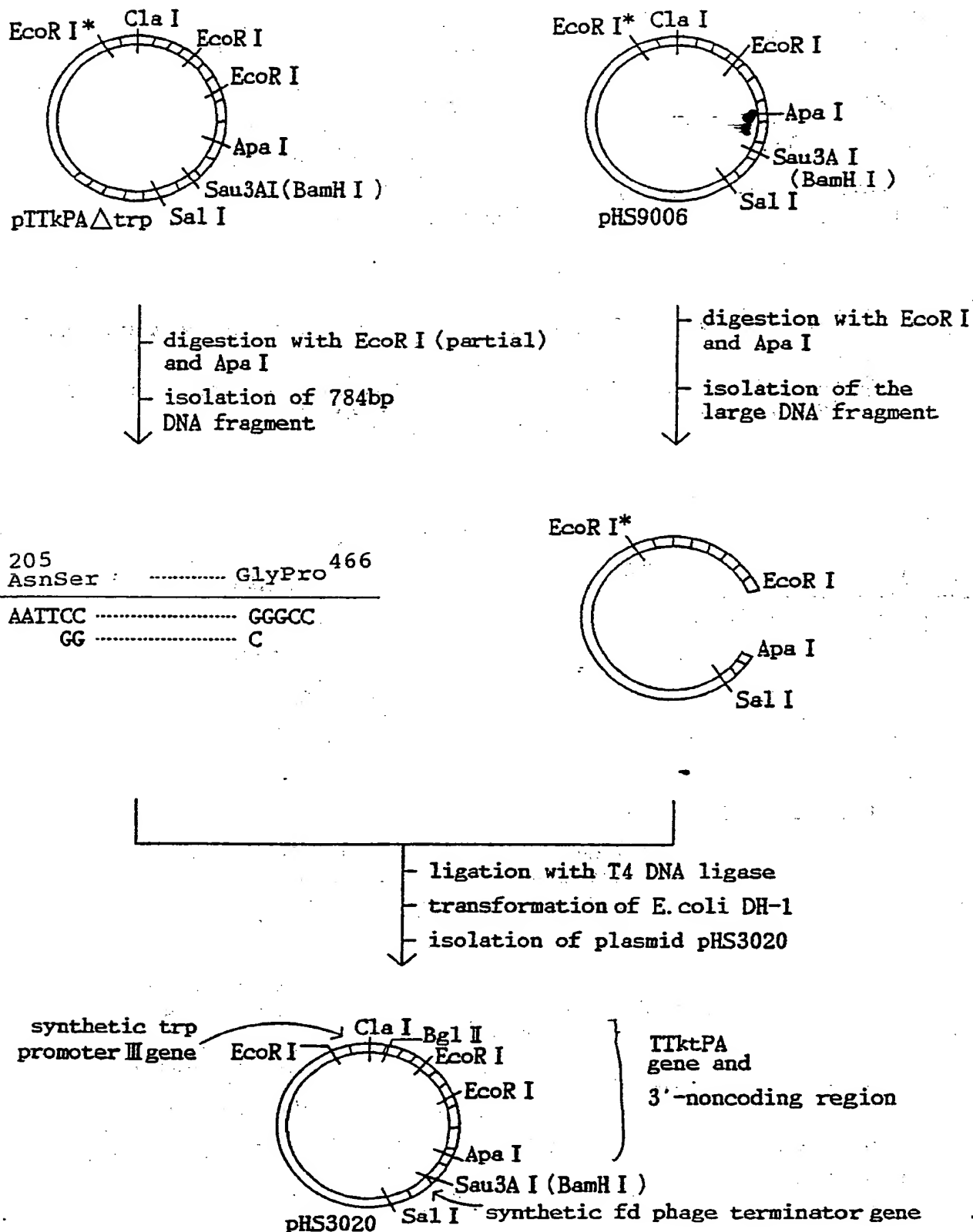


Fig. 26. Construction and cloning of plasmid pmTTk

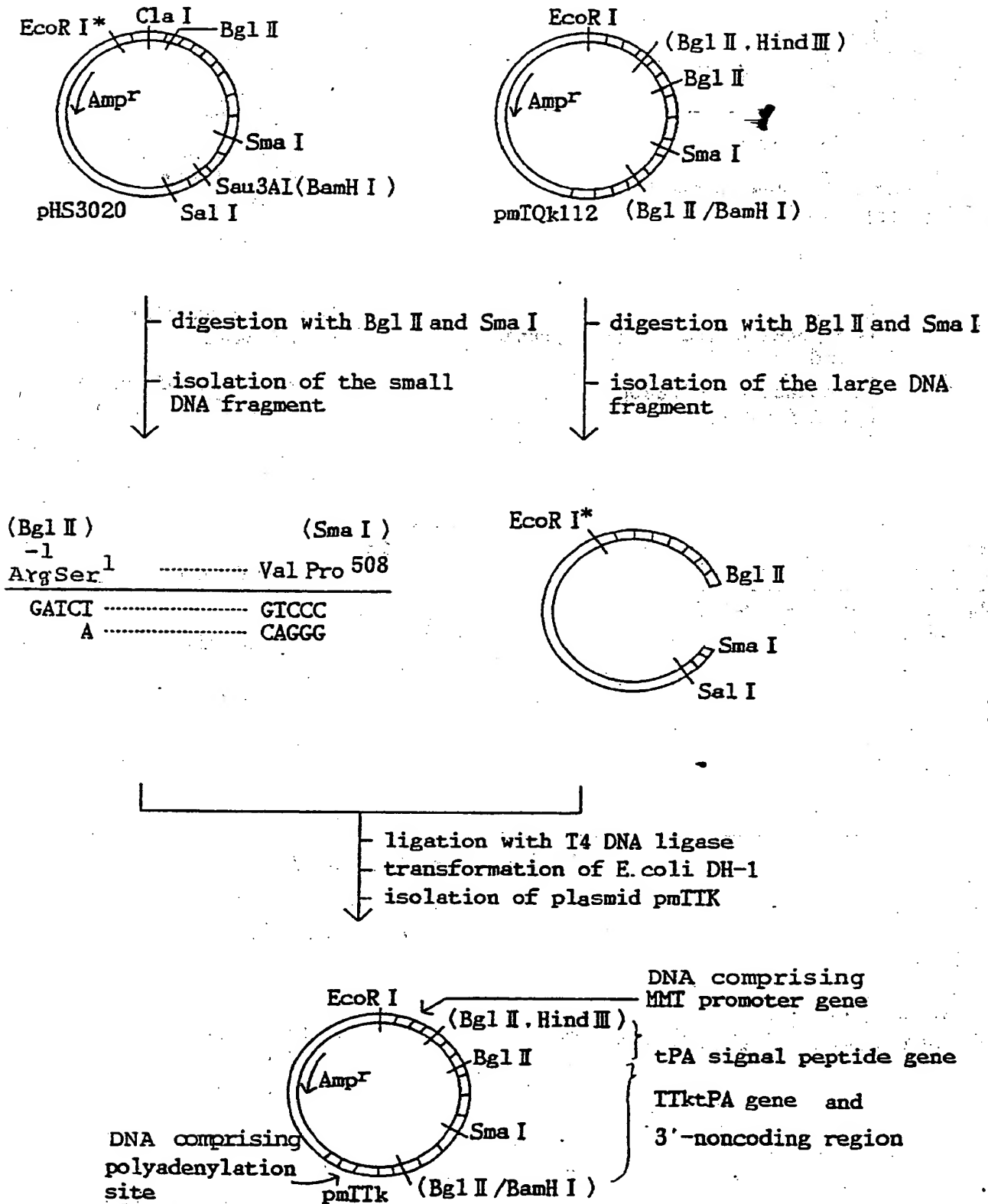


Fig. 27. Construction and cloning of plasmid pMH3025

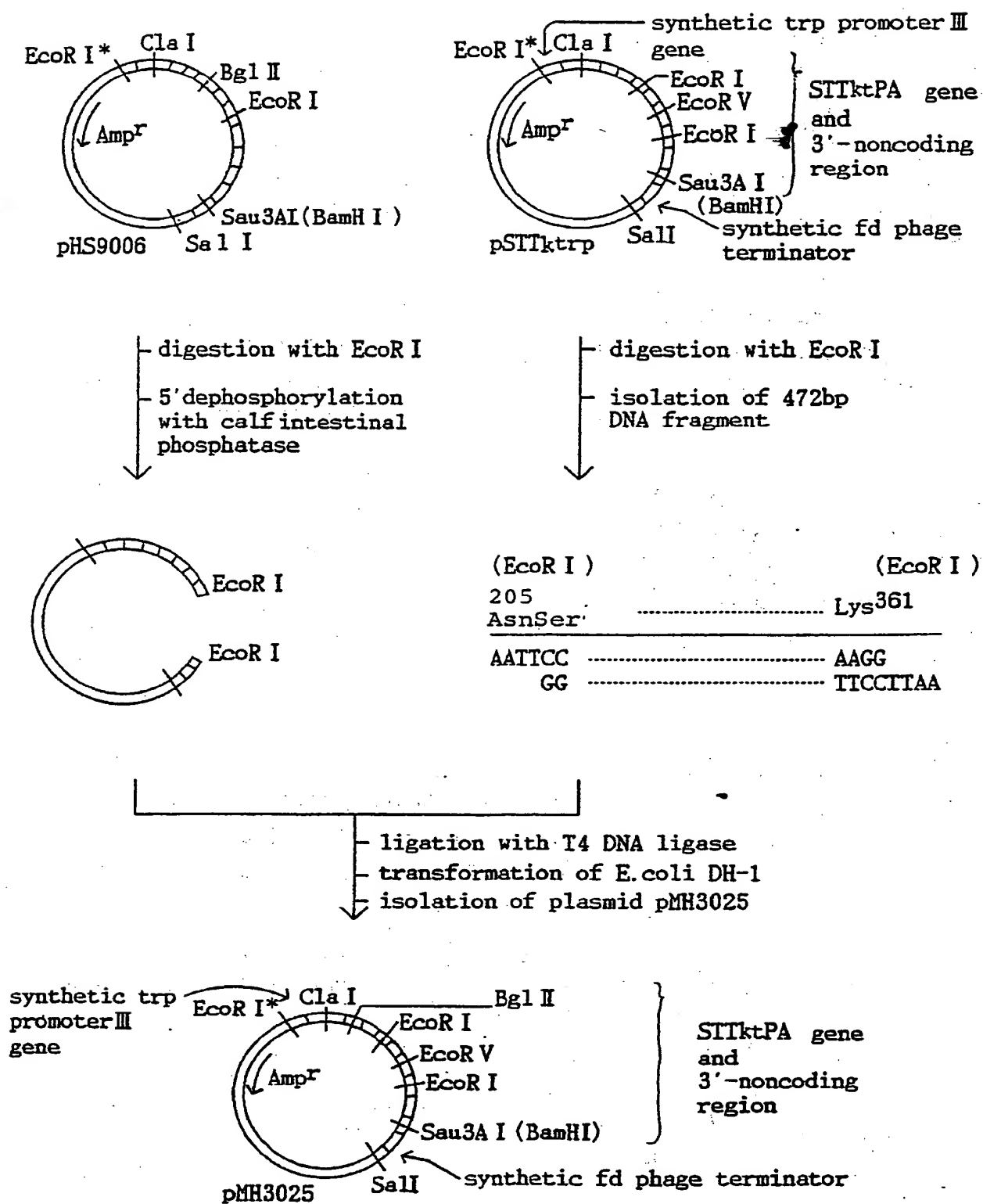


Fig. 28. Construction and cloning of plasmid pmSTTk

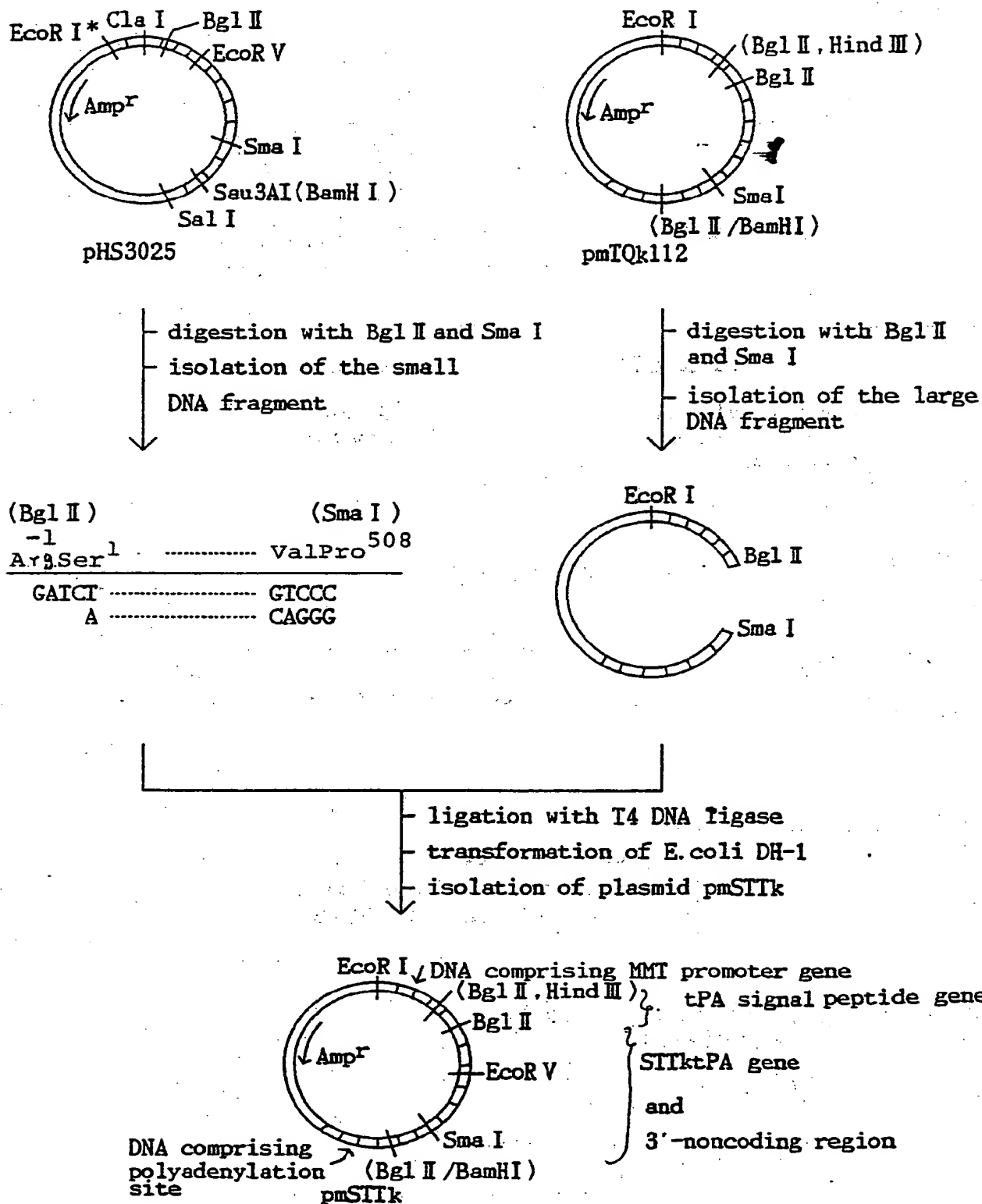


Fig. 29. DNA Sequence of coding region in pTTkPAΔtrp

(Upper: Coding chain

Lower: Coded amino acid sequence)

```

5' -ATGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGAC
MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
      TTK+PA
      70      80      90      100      110      120
AGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGGAATCCATGATCCTGATAGGCAAG
SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys
      130      140      150      160      170      180
GTTTACACAGCACAGAACCCAGTGCCAGGCACTGGGCCTGGGCAAACATAATTACTGC
ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys
      190      200      210      220      230      240
CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACG
ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr
      250      260      270      280      290      300
TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCT
TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnPro
      310      320      330      340      350      360
CAGTTTCGCATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCC
GlnPheArgIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAla
      370      380      390      400      410      420
ATCTTTGCCAAGCACAGGAGGTCCGCCGAGAGCGGTTCTGTGCGGGGGCATACTCATC
IlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIle
      430      440      450      460      470      480
AGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAC
SerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHis
      490      500      510      520      530      540
CTGACCGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTT
LeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPhe
      550      560      570      580      590      600
GAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATT
GluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIle
      610      620      630      640      650      660
GCGCTGCTGCAGCTGAAATCGGATTGCTCCCGCTGTGCCAGGAGAGCAGCGTGGTCCGC
AlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArg
      670      680      690      700      710      720
ACTGTGTGCTTCCCGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCC
ThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSer
      730      740      750      760      770      780
GGCTACGSCAAGCATGAGGCCTTGTCTCTTTCTATTCCGAGCGGCTGAAGGAGGCTCAT
GlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHis
      790      800      810      820      830      840
GTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACC
ValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThr
      850      860      870      880      890      900
GACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGGCCCAAGGCAAACCTGCACGAC
AspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAsp
      910      920      930      940      950      960
GCCTGCCAGGGCGATTCCGGAGGCCCTGGTGTGTCTGAACGATGCCCGCATGACTTTG
AlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeu
      970      980      990      1000      1010      1020
GTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACA
ValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThr
      1030      1040      1050      1060      1070
AAGGTTACCAACTACCTAGACTGGATTGCTGACAACATGCGACCGTGA -3'
LysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***

```

Fig. 30. DNA sequence of coding region in pTTiPAΔtrp

(Upper: Coding chain

Lower: Coded amino acid sequence)

```

5' - ATGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCAGGCAC
MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
      10      20      30      40      50      60
      TTTtPA
      70      80      90      100     110     120
AGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGAATTCATGATCCTGATAGGCAAG
SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys
      130     140     150     160     170     180
GTTTACACAGCACAGAACCCAGTGCCTCAGGCACTGGGCTGGGCAACATAATTACTGC
ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys
      190     200     210     220     230     240
CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCAGGCTGACG
ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr
      250     260     270     280     290     300
TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCT
TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnPro
      310     320     330     340     350     360
CAGTTTCGCATCATAGGAGGCCTCTCGCCGACATCGCCTCCACCCCTGGCAGGCTGCC
GlnPheArgIleIleGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAla
      370     380     390     400     410     420
ATCTTTGCCAAGCACAGGAGGTGCGCCGAGAGCGGTTCTGTGCGGGGCATACTCATC
IlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIle
      430     440     450     460     470     480
AGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAC
SerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHis
      490     500     510     520     530     540
CTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAAAATTT
LeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGlnLysPhe
      550     560     570     580     590     600
GAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATT
GluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIle
      610     620     630     640     650     660
GCGCTGCTGCAGCTGAAATCGGATTCTCCCGCTGTGCCAGGAGAGCAGCGTGGTCCGC
AlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArg
      670     680     690     700     710     720
ACTGTGTGCTTCCCCGGCGGACCTGCAGCTGCCCGACTGGACGGAAGTGTGAGCTCTCC
ThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSer
      730     740     750     760     770     780
GGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCCGAGCGGCTGAAGGAGGCTCAT
GlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHis
      790     800     810     820     830     840
GTCAGACTGTATCCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACC
ValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThr
      850     860     870     880     890     900
GACAACATGCTGTGTGCTGAGACACTCGGAGCGGCGGCCCCAGGCAAACTTGCACGAC
AspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAsp
      910     920     930     940     950     960
GCCTGCCAGGCGGATTCCGGAGGCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTG
AlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeu
      970     980     990     1000    1010    1020
GTGGGCATCATCAGCTGGGCTGGGCTGTGGACAGAAGGATGTCCCGGTGTGTACACA
ValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThr
      1030    1040    1050    1060    1070
AAGGTTACCAACTACCTAGACTGGATTCTGTGACAACATGCGACCGTGA - 3'
LysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***

```


Fig. 31. DNA sequence of coding region in pTQkPAΔtrp
(Upper: Coding chain, Lower: Coded amino acid sequence)

```

5' - ATGTGTTATGAGGACCAGGCATCAGCTACAGGGCAGCTGGAGCACAGCGGAGAGTGGC
MetCysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGly
      TQkPA
      70      80      90      100      110      120
GCGGAGTGACCAACTGGAACAGCAGCGGCTGGCCAGAACCCCTACAGCGGGCGGAGG
AlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArg
      130      140      150      160      170      180
CCAGACGCCATCAGGCTGGGCTGGGGAACCACTACTGCAGAAACCCAGATCGAGAC
ProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAsp
      190      200      210      220      230      240
TCAAAGCCCTGGTGTCTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACC
SerLysProTrpCysTyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThr
      250      260      270      280      290      300
CCTGCCTGCTCTGAGGGAACAGTGACTGCTACTTTGGGAATGGGTCCAGCCTACCGTGGC
ProAlaCysSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGly
      310      320      330      340      350      360
ACGCACAGCCTCACCGAGTGGGTGCCTCCTGCCCTCCCGTGGAAATCCATGATCCTGATA
ThrHisSerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIle
      370      380      390      400      410      420
GGCAAGGTTTACACAGCACAGAACCCCACTGCCAGGCACTGGGCTGGGCAACATAAT
GlyLysValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsn
      430      440      450      460      470      480
TACTGCCGAATCCTGATGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGG
TyrCysArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArg
      490      500      510      520      530      540
CTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGGGCTGAGACAGTACAGC
LeuThrTrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSer
      550      560      570      580      590      600
CAGCCTCAGTTTCGCATCAAAGGAGGGCTCTTCGCCGACATCCCTCCACCCCTGGCAG
GlnProGlnPheArgIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGln
      610      620      630      640      650      660
GCTGCCATCTTTGCCAAGCACAGGAGGTGCGCCGGAGAGCGGTTCTGTGCGGGGGCATA
AlaAlaIlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIle
      670      680      690      700      710      720
CTCATCAGCTCCTGCTGGATTCTCTGCGCCCACTGCTCCAGGAGAGGTTTCCGCCC
LeuIleSerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProPro
      730      740      750      760      770      780
CACCACCTGACGGTGATCTTGGGCAGAACATACCGGTGGTCCCTGGCGAGGAGGAGCAG
HisHisLeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGln
      790      800      810      820      830      840
AAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAAT
LysPheGluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsn
      850      860      870      880      890      900
GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCAGGAGACGCGTG
AspIleAlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerVal
      910      920      930      940      950      960
GTCCGCACTGTGTGCTTCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAG
ValArgThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGlu
      970      980      990      1000      1010      1020
CTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCTTTCTATTCCGAGCGGCTGAAGGAG
LeuSerGlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGlu
      1030      1040      1050      1060      1070      1080
GCTCATGTACAGACTGTACCCATCCAGCCGCTGCACATCACAACATTACTTAACAGAACA
AlaHisValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThr
      1090      1100      1110      1120      1130      1140
GTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGGGCCCCAGGCAAACTTG
ValThrAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeu
      1150      1160      1170      1180      1190      1200
CACGACGCGCTGCCAGGGCGATTCCGGAGGGCCCCCTGGTGTGTCTGAACGATGGCCGATG
HisAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMet
      1210      1220      1230      1240      1250      126
ACTTTGGTGGCATCATCAGCTGGGCTGGGCTGTGGACAGAAGGATGTCCCGGTGTG
ThrLeuValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyVal
      1270      1280      1290      1300      1310
TACACAAAGGTTACCAACTACCTAGACTGGATTCTGACAACATGCCGACCGTGA - 3'
TyrThrLysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro...

```

Fig. 32. DNA sequence of coding region in *pTQiPAA_{trp}*
(Upper: Coding chain, Lower: Coded amino acid sequence)

```

5' - ATGTGTTATGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGC
MetCysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGly
  ↳ TQiPAA
      70      80      90      100     110     120
GCCGAGTGCACCAACTGGAACAGCAGCGCGTTGGCCCAAGCCCTACAGCGGCGGAGG
AlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArg

      130     140     150     160     170     180
CCAGACGCCATCAGGCTGGGCTGGGGAACCACTACTGCAGAAACCCAGATCGAGAC
ProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAsp

      190     200     210     220     230     240
TCAAAGCCCTGGTGTCTACGTCTTTAAGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACC
SerLysProTrpCysTyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThr

      250     260     270     280     290     300
CCTGCCTGCTCTGAGGGAACAGTGAATGCTACTTTGGGAATGGGTGAGCTACCGTGGC
ProAlaCysSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGly

      310     320     330     340     350     360
ACGCACAGCCTCACCAGTCCGGTGCCTGCGTCCCGTGAATTCATGATCCTGATA
ThrHisSerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIle

      370     380     390     400     410     420
GGCAAGGTTTACACAGCACAGAACCCAGTGGCCAGGCACTGGGCTGGGCAACATAAT
GlyLysValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsn

      430     440     450     460     470     480
TACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCACGTGCTGAAGAACCGCAGG
TyrCysArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArg

      490     500     510     520     530     540
CTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCTGAGACAGTACAGC
LeuThrTrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSer

      550     560     570     580     590     600
CAGCCACAGTTTCGCATCATAGGAGGCTCTTCGCGGACATCGGCTCCACCCCTGGCAG
GlnProGlnPheArgIleIleGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGln

      610     620     630     640     650     660
GCTGCCATCTTTGCCAAGCACAGGAGGTGCGCCGGAGAGCGGTTCTGTGCGGGGGCATA
AlaAlaIlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIle

      670     680     690     700     710     720
CTCATCAGCTCCTGCTGGATTCTCTGCGCGCCCACTGCTTCCAGGAGAGGTTTCCGCCC
LeuIleSerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProPro

      730     740     750     760     770     780
CACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAG
HisHisLeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGln

      790     800     810     820     830     840
AAATTGAACTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAAT
LysPheGluValGluLysTyrIleValHisLysGluPheAspAspThrTyrAspAsn

      850     860     870     880     890     900
GACATTGCGTGTCTGCACTGAAATCGGATTCTGCCGCTGTGCCCAAGGAGAGCAGCGTG
AspIleAlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerVal

      910     920     930     940     950     960
GTCCGCACTGTGTGCTTCCCGGGCGGACCTGCAGCTGCCGGAAGTGGAGTGTGAG
ValArgThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGlu

      970     980     990     1000    1010    1020
CTCTCCGGCTACGGCAAGCATGAGGCTTGTCTCCTTCTATTCCGAGCGGCTGAAGGAG
LeuSerGlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGlu

      1030    1040    1050    1060    1070    1080
GCTCATGTACAGACTGTACCCATCCAGCGCTGCACATCACAACTTTACTTAACAGAACA
AlaHisValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThr

      1090    1100    1110    1120    1130    1140
GTCACCGACAAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGCCCCAGGCAAACTTG
ValThrAspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeu

      1150    1160    1170    1180    1190    1200
CACGACGCTGCCAAGGCGGATTCCGGAGGCCCCCTGGTGTCTGAACGATGGCCGCTATG
HisAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMet

      1210    1220    1230    1240    1250    1260
ACTTTGGTGGCATCATCAGCTGGGCGCTGGGCTGTGGACAGAAGGATGTCGCGGTGTG
ThrLeuValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyVal

      1270    1280    1290    1300    1310
TACACAAAGGTTACCAACTACCTAGACTGGATTCTGTGACAACATGCCACCGTGA -3'
TyrThrLysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
  ↳

```

Fig. 33. DNA sequence of coding region in pSTTkt_{trp}
 (Upper: Coding chain
 Lower: Coded amino acid sequence)

```

5' -ATGTCCTGAGGGAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCAGGCAC
MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
  ↳ STTktPA
      10      20      30      40      50      60
AGCCTCACCAGTGGGTGCTCTGCTCCCGTGAATTCATGATCCTGATAGGCAAG
SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys
      70      80      90      100     110     120
GTTTACACAGCAGAGAACCCAGTGGCCAGGCACTGGGCTGGGCAAACATAATTACTGC
ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys
      130     140     150     160     170     180
CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCAGGCTGACG
ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr
      190     200     210     220     230     240
TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCTGAGACAGTACAGCCAGCCA
TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnPro
      250     260     270     280     290     300
CAGTTTGATATCAAAGGAGGCCTCTCGCCGACATCGCCTCCACCCCTGGCAGGCTGCC
GlnPheAspIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAla
      310     320     330     340     350     360
ATCTTTGCCAAGCACAGGAGGTGCGCCGGAGAGCGGTTCTGTGCGGGGGCATACTCATC
IlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIle
      370     380     390     400     410     420
AGCTCCTGCTGGATTCTCTGCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAC
SerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHis
      430     440     450     460     470     480
CTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTT
LeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPhe
      490     500     510     520     530     540
GAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACATGACATT
GluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIle
      550     560     570     580     590     600
GCGCTGCTGCAGCTGAAATCGGATTCTCCCGCTGTGCCAGGAGAGCAGCGTGGTCCGC
AlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArg
      610     620     630     640     650     660
ACTGTGTGCTTCCCCCGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCC
ThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSer
      670     680     690     700     710     720
GGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCCGAGCGGCTGAAGGAGGCTCAT
GlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHis
      730     740     750     760     770     780
GTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACC
ValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThr
      790     800     810     820     830     840
GACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACCTGCACGAC
AspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAsp
      850     860     870     880     890     900
GCCTGCCAGGGCGATTTCGGGAGGCCCTTGGTGTGTCTGAACGATGGCCGATGACTTTG
AlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeu
      910     920     930     940     950     960
GTGGGCATCATCAGCTGGGCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACA
ValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThr
      970     980     990     1000    1010    1020
AAGGTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGA -3'
LysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
  
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Fig. 34. DNA sequence of coding region in pSTQktrp
(Upper: Coding chain
Lower: Coded amino acid sequence)

```

5' - ATGTTGTTATGAGGACCACTGGAACAGCAGCGCTTGGCCAGAAAGCCCTACAGCGGGCGGAGG
MetCysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGly
  ↳ STQKtPA
  70- 80 90 100 110 120
GCCGAGTGCACCACTGGAACAGCAGCGCTTGGCCAGAAAGCCCTACAGCGGGCGGAGG
AlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArg
  130 140 150 160 170 180
CCAGACGCCATCAGGCTGGGCTGGGGAACCACTACTGCAGAAACCCAGATCGGAC
ProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAsp
  190 200 210 220 230 240
TCAAAGCCCTGGTGTCTACGCTTTAAGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACC
SerLysProTrpCysTyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThr
  250 260 270 280 290 300
CCTGCCTGCTCTGAGGGAACAGTGACTGCTACTTTGGGAATGGGTGAGCCTACCGTGGC
ProAlaCysSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGly
  310 320 330 340 350 360
ACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGAATTCATGATCCTGATA
ThrHisSerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIle
  370 380 390 400 410 420
GGCAAGGTTTACACAGCACAGAACCCAGTGGCCAGGCACTGGGCTGGGCAAAACATAAT
GlyLysValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsn
  430 440 450 460 470 480
TACTGCCGGAATCTGATGGGGATGCCAAGCCCTGGTCCACGTGCTGAAGAACCAGCAGG
TyrCysArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArg
  490 500 510 520 530 540
CTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGGGCGCTGAGACAGTACAGC
LeuThrTrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSer
  550 560 570 580 590 600
CAGCCACAGTTTATATCAAAGGAGGCTGTTCCCGGACATCGCCTCCACCCCTGGCAG
GlnProGlnPheAspIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGln
  610 620 630 640 650 660
GCTGCCATCTTTGCCAAGCACAGGAGGTGCGCCGGAGAGCGGTTCTGTGCGGGGGCATA
AlaAlaIlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIle
  670 680 690 700 710 720
CTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCC
LeuIleSerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProPro
  730 740 750 760 770 780
CACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAG
HisHisLeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGln
  790 800 810 820 830 840
AAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAAT
LysPheGluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsn
  850 860 870 880 890 900
GACATTGCGCTGCTGCAGCTGAAATCGGATTCTGCTCCCGTGTGCCAGGAGAGCAGCGTG
AspIleAlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerVal
  910 920 930 940 950 960
GTCCGCACTGTGTGCTTCCCGCGGGACCTGCAGCTGCCGAGTGGCAGGAGTGTGAG
ValArgThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGlu
  970 980 990 1000 1010 1020
GTCTCCGCTACGCAAGCATGAGGCGTGTCTCTTCTATTCCGAGCGGCTGAAGGAG
LeuSerGlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGlu
  1030 1040 1050 1060 1070 1080
GCTCATGTACAGTGTACCCATCCAGCGCTGCACATCACAACATTTACTTAACAGAACA
AlaHisValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThr
  1090 1100 1110 1120 1130 1140
GTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGCCCCAGGCAAACTTG
ValThrAspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeu
  1150 1160 1170 1180 1190 1200
CACGACGCTGCCAGGCGATTCCGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCTG
HisAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMet
  1210 1220 1230 1240 1250 1260
ACTTTGGTGGCATCATCAGCTGGGCGCTGGGCTGTGGACAGAAGGATGTCGCGGCTGTG
ThrLeuValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyVal
  1270 1280 1290 1300 1310
TACACAAAGGTTACCAACTACCTAGACTGGATTGCGTACAACATCCGACCGTGA -3'
TyrThrLysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro...

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Fig. 35. DNA sequence of coding region in pSTQitrp
(Upper: Coding chain
Lower: Coded amino acid sequence)

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5' - ATGTGTTATGAGGACCAAGGGCATCAGCTACAGGGGCAGTGGAGCACAGCGGAGAGTGGC
MetCysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGly
  ↳ STQitPA
    70 80 90 100 110 120
GCCGAGTGCACCAACTGGAACAGCAGCGCGTTGGCCCAAGCCCTACAGCGGGCGGAGG
AlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArg

    130 140 150 160 170 180
CCAGACGGCATCAGGCTGGGCTGGGGAACCACTACTGCAGAAACCCAGATCGAGAC
ProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAsp

    190 200 210 220 230 240
TCAAAGCCCTGGTGTCTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACC
SerLysProTrpCysTyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThr

    250 260 270 280 290 300
CCTGCTGCTCTGAGGGAACAGTGAAGTCTCTTTGGGAATGGGTGAGCTACCGTGGC
ProAlaCysSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGly

    310 320 330 340 350 360
ACGCACAGCCTCAGCGAGTGGGTGCTCTGCTCCCTCCCGTGAATTCATGATCCTGATA
ThrHisSerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIle

    370 380 390 400 410 420
GGCAAGGTTTACACAGCACAGAACCCAGTGGCCAGGCACTGGGCGTGGGCAACATAAT
GlyLysValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsn

    430 440 450 460 470 480
TACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGGCACGTGCTGAAGAACCGCAGG
TyrCysArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArg

    490 500 510 520 530 540
CTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCCGCGCTGAGACAGTACAGC
LeuThrTrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSer

    550 560 570 580 590 600
CAGCCACAGTTTGATATCATAGGAGGCTCTTCGCGGACATCGCCTCCACCCCTGGCAG
GlnProGlnPheAspIleIleGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGln

    610 620 630 640 650 660
GCTGCCATCTTTGGCAAGCACAGGAGGTGCGCCGGAGAGCGGTTCTGTGCGGGGGCATA
AlaAlaIlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIle

    670 680 690 700 710 720
CTCATCAGCTCCTGCTGATCTCTCTGCGCGCCCACTGCTTCCAGGAGAGGTTTCCGCCC
LeuIleSerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProPro

    730 740 750 760 770 780
CACCACCTGACGGTGTATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAG
HisHisLeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGln

    790 800 810 820 830 840
AAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAAAT
LysPheGlyValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsn

    850 860 870 880 890 900
GACATTGCGCTGCTGCAAGTGAATCGGATTCTGCTCCCGCTGTGCCAGGAGAGCAGCGTG
AspIleAlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerVal

    910 920 930 940 950 960
GTCCGCACTGTGTGCCTTCCCGCGGGACCTGCAGCTGCCGGAAGTGGAGTGTGAG
ValArgThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGlu

    970 980 990 1000 1010 1020
CTCTCCGCTACGGCAAGCATGAGGCCCTTGTCTCTTCTATTCCGAGCGGCTGAAGGAG
LeuSerGlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGlu

    1030 1040 1050 1060 1070 1080
GCTCATGTCTGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACA
AlaHisValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThr

    1090 1100 1110 1120 1130 1140
GTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGCCCCAGGCAAACTTG
ValThrAspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeu

    1150 1160 1170 1180 1190 1200
CAGCAGCGCTGCCAGGGCGATTCCGGAGGCGCCCTGGTGTGTCTGAACGATGGCCGCTATG
HisAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMet

    1210 1220 1230 1240 1250 1260
ACTTTGTGGGCATCATCAGCTGGGGCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTG
ThrLeuValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyVal

    1270 1280 1290 1300 1310
TACACAAAGGTTACCAACTACCTAGACTGGATTCTGACAACATGCGACCGTGA -3'
TyrThrLysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
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Fig. 36. DNA sequence of coding region in puTTtrp
 (Upper: Coding chain
 Lower: Coded amino acid sequence)

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5' -ATGTCCTGAGGGAAACAGTGAAGTCTACTTTGGGAATGGGTGAGCCTACCGTGGCAGGCAC
MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
  ↳ uTT+PA
      70      80      90      100     110     120
AGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGAATTCCATGATCCTGATAGGCAAG
SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys
      130     140     150     160     170     180
GTTTACACAGCACAGAACCCAGTGGCCAGGCACTGGGCTGGGCAAACATAATTACTGC
ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys
      190     200     210     220     230     240
CGGAATCCTGATGGGGATGCCAAGCCCTGGTCCACGTGCTGAAGAACCGCAGGCTGACG
ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr
      250     260     270     280     290     300
TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGACTCTGCGTCCG
TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnThrLeuArgPro
      310     320     330     340     350     360
CGGTTCAAATCAAAGGAGGCCTCTTCGCCGACATCGCCTCCACCCCTGGCAGGCTGCC
ArgPheLysIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAla
      370     380     390     400     410     420
ATCTTTGCCAAGCACAGGAGGTGCGCCGGAGAGCGGTTCTGTGCGGGGGCATACTCATC
IlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIle
      430     440     450     460     470     480
AGCTCCTGCTGGATTCTCTCTGCCGCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAC
SerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHis
      490     500     510     520     530     540
CTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATT
LeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGlnLysPhe
      550     560     570     580     590     600
GAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATT
GluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIle
      610     620     630     640     650     660
GCGCTGCTGCAGCTGAAATCGGATTCTGCTCCCGCTGTGCCAGGAGAGCAGCGTGGTCCGC
AlaLeuLeuGlnLeuLysSerAspSerArgCysAlaGlnGluSerSerValValArg
      670     680     690     700     710     720
ACTGTGTGCTTCCCCCGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCC
ThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSer
      730     740     750     760     770     780
GGCTACGGCAAGCATGAGGCCTTGTCTCTTCTATTCCGAGCGGCTGAAGGAGGCTCAT
GlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHis
      790     800     810     820     830     840
GTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACC
ValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThr
      850     860     870     880     890     900
GACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGCCAGGCAAACTTGCACGAC
AspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAsp
      910     920     930     940     950     960
GCCTGCCAGGGCGATTCCGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTG
AlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeu
      970     980     990     1000    1010    1020
GTGGGCATCATCAGCTGGGCGCTGGGACAGAAAGGATGTCCCGGGTGTGTATACACA
ValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThr
      1030    1040    1050    1060    1070
AAGGTTACCAACTACCTAGACTGGATTCTGTGACAACATGCCGACCGTGA -3'
LysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
  ↳

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Fig. 37. DNA sequence of coding region in pthTTtrp

(Upper: Coding chain, Lower: Coded amino acid sequence)

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      10      20      30      40      50      60
5' -ATGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCAGCGCAC
MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
      70      80      90     100     110     120
      ↳ thTTtPA
AGCCTCACCGAGTCGGGTGCCTCCTGCCCTCCCGTGAATTCCATGATCCTGATAGGCAAG
SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys
     130     140     150     160     170     180
GTTTACACAGCACAGAACCCAGTGCCAGGCACTGGGCTGGGCAAACATAATTACTGC
ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys
     190     200     210     220     230     240
CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACG
ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr
     250     260     270     280     290     300
TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCTGAGACAGTACAGCCAGCCA
TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnPro
     310     320     330     340     350     360
ATTCTAGATCTGGAGGCCTCTTCGCCGACATCGCCTCCACCCCTGGCAGGCTGCCATG
IleProArgSerGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIle
     370     380     390     400     410     420
TTTGCCAAGCACAGGAGGTGCGCCGGAGAGCGGTTCTGTGCGGGGGCATACTCATCAGC
PheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSer
     430     440     450     460     470     480
TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTG
SerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisLeu
     490     500     510     520     530     540
ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAA
ThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPheGlu
     550     560     570     580     590     600
GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
ValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAla
     610     620     630     640     650     660
CTGCTGCAGCTGAAATCGGATTTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACT
LeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThr
     670     680     690     700     710     720
GTGTGCCCTTCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGC
ValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGly
     730     740     750     760     770     780
TACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTC
TyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisVal
     790     800     810     820     830     840
AGACTGTACCCATCCAGCCGCTGCACATCACAACATTACTTAACAGAACAGTCACCGAC
ArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAsp
     850     860     870     880     890     900
AACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGGCCCCAGGCAAACTTGCACGACGCC
AsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAla
     910     920     930     940     950     960
TGCCAGGGCGATTTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG
CysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuVal
     970     980     990     1000     1010     1020
GGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG
GlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLys
     1030     1040     1050     1060
GTTACCAACTACCTAGACTGGATTCTGTGACAACATGCGACCGTGA -3'
ValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
      ↳

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Fig. 38. DNA sequence of coding region in pmTQk112

(Upper: Coding chain

Lower: Coded amino acid sequence)

```

5' - ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTT
    MetAspAlaMetLysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal

    10      20      30      40      50      60
    TCGCCAGCCAGGAAATCCATGCCGATTGAGAAGAGGAGCCAGATCTTGCTACGAGGAC
    SerProSerGlnGluIleHisAlaArgPheArgArgGlyAlaArgSerCysTyrGluAsp
    70      80      90      100     110     120
    CAGGGCATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGCGCCGAGTGCACAC
    GlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGlyAlaGluCysThrAsn
    130     140     150     160     170     180
    TGGAAACAGCAGCGCTTGGCCAGAAAGCCCTACAGCGGGGAGGCCAGCCATCAGG
    TrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArgProAspAlaIleArg
    190     200     210     220     230     240
    CTGGGCTGGGGAACCAACTACTGCAGAAACCCAGATCGAGACTCAAAGCCCTGGTGC
    LeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAspSerLysProTrpCys
    250     260     270     280     290     300
    TACGTCTTTAAGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACCCCTGCCTGCTCTGAG
    TyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThrProAlaCysSerGlu
    310     320     330     340     350     360
    GGAACAGTGACTGCTACTTTGGGAATGGGTGAGCCTACCGTGGCAGGCACAGCCTCACC
    GlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSerLeuThr
    370     380     390     400     410     420
    CAGTCGGGTGCCTCCTGCTCCCGTGGAAATCCATGATCCTGATAGCAAGGTTTACACA
    GluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysValTyrThr
    430     440     450     460     470     480
    GCACAGAACCCAGTGGCCAGGCACTGGGCGTGGGCAAAACATAATTACTGCCGGAATCCT
    AlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnPro
    490     500     510     520     530     540
    GATGGGATGCCAAGCCCTGGTCCACCTGCTGAAGAACCAGCAGGCTGACGTGGGAGTAC
    AspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyr
    550     560     570     580     590     600
    TGTGATGTGCCCTCCTGCTCCACCTGGCGCCTGAGACAGTACAGCCAGCCTCAGTTTCGC
    CysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArg
    610     620     630     640     650     660
    ATCAAAGGAGGGCTCTTCGCGGACATCGCCTCCACCCCTGGCAGGCTGCCATCTTTGCC
    IleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAla
    670     680     690     700     710     720
    AAGCACAGGAGTTCGCGCGGAGAGCGGTTCTGTGCGGGGGCATACTCATCAGCTCCTGC
    LysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCys
    730     740     750     760     770     780
    TGGATTCTCTGCGCGCCACTGCTTCCAGGAGAGGTTTCCGCGCCACCTGACGGTGTG
    TrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrVal
    790     800     810     820     830     840
    ATCTTGGGCAGAACATACCGGCTGGTCCCTGCGGAGGAGGAGCAGAAATTTGAAGTCGAA
    IleLeuGlyArgThrTyrArgValValProGlyGluGluGlnLysPheGluValGlu
    850     860     870     880     890     900
    AAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTG
    LysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAlaLeuLeu
    910     920     930     940     950     960
    CAGCTGAAATCGGATTGCTCCCGCTGTGCCAGGAGAGCAGCGTGCTCCGCACTGTGTGC
    GlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCys
    970     980     990     1000    1010    1020
    CTTCCCGCGCGGACCTGCAGCTGCCGACTGGACCGAGTGTGAGCTCTCCGGCTACGGC
    LeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGly
    1030    1040    1050    1060    1070    1080
    AAGCATGAGGCCCTTGTCTCTTTCTATTCCGAGCGGCTGAAGGAGGCTCATGTCCAGACTG
    LysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeu
    1090    1100    1110    1120    1130    1140
    TACCCATCCAGCCGCTGACATCACAACATTACTTAACAGAACAGTCACCGACAACATG
    TyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMet
    1150    1160    1170    1180    1190    1200
    CTGTGTGCTGGAGACACTCGGAGCGCGCGGCCCCAGGCAAACTTGACGACGCTGCCAG
    LeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGln
    1210    1220    1230    1240    1250    1260
    GCGGATTCCGGAGGCGCCCTGGTGTGTCTGAACGATCGCCGATGACTTTGGTGGGCATC
    GlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIle
    1270    1280    1290    1300    1310    1320
    ATCAGCTGGGGCCTCGGCTGTGGACAGAAGGATGTCCGGGTGTGTACACAAAGGTTACC
    IleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThr
    1330    1340    1350    1360    1370    1380
    AACTACCTAGACTGGATTCTGTGACAACATCGGACCGTGA - 3'
    AsnTyrLeuAspTrpIleArgAspAsnMetArgPro...
  
```


Fig. 39. DNA sequence of coding region in pmTTk
(Upper: Coding chain
Lower: Coded amino acid sequence)

```

5' - ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCAGTCTTCGTT
MetAspAlaMetLysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal

      70      80      90      100      110      120
TCGCCCAGCCAGGAAATCCATGCCCGATTGAGAAGAGGAGCCAGATCTGAGGGAACAGT
SerProSerGlnGluIleHisAlaArgPheArgArgGlyAlaArgSerGluGlyAsnSer
      130      140      150      160      170      180
GACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCAGCCAGCCTCACCAGTCCGGGT
AspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSerLeuThrGluSerGly
      190      200      210      220      230      240
GCCTCCTGCCTCCCGTGGAAATCCATGATCCTGATAGGCAAGGTTTACACAGCACAGAAC
AlaSerCysLeuProTrpCysMetIleLeuIleGlyLysValTyrThrAlaGlnAsn
      250      260      270      280      290      300
CCCAGTGGCCAGGCACTGGGCTGGGCAAACATAATTACTGCCGAATCCTGATGGGGAT
ProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnProAspGlyAsp
      310      320      330      340      350      360
GCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGTGTG
AlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCysAspVal
      370      380      390      400      410      420
CCCTCCTGCTCCACCTGCGGCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAGGA
ProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArgIleLysGly
      430      440      450      460      470      480
GGGCTCTTCGCCGACATCGCCTCCACCCCTGGCAGGCTGCCATCTTTGCCAAGCACAGG
GlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLysHisArg
      490      500      510      520      530      540
AGGTCGCCCCGAGAGCGGTTCTCTGTGCGGGGGCATACTCATCAGCTCCTGTGTGATTCTC
ArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrpIleLeu
      550      560      570      580      590      600
TCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACTGACGGTGATCTTGGGC
SerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIleLeuGly
      610      620      630      640      650      660
AGAACATACCGGGTGGTCCCTGGCGAGGAGCAGAAATTGAAGTCGAAAAATACATT
ArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLysTyrIle
      670      680      690      700      710      720
GTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAA
ValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAlaLeuLeuGlnLeuLys
      730      740      750      760      770      780
TCGGATTCTCCCGCTGTGCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCTTCCCCCG
SerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCysLeuProPro
      790      800      810      820      830      840
GCGGACCTGCAGCTGCCCGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAG
AlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGlyLysHisGlu
      850      860      870      880      890      900
GCCTTGCTCTCTTTCTATTCCGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCC
AlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeuTyrProSer
      910      920      930      940      950      960
AGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCT
SerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMetLeuCysAla
      970      980      990      1000      1010      1020
GGAGACACTCGGAGCGCGGCGCCAGGCAAACTTGCACGACGCTGCCAGGGCGATTGCG
GlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGlnGlyAspSer
      1030      1040      1050      1060      1070      1080
GGAGGCCCCCTGGTGTGTCTGAACGATGCCCGCATGACTTTGGTGGGCATCATCAGCTGG
GlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIleIleSerTrp
      1090      1100      1110      1120      1130      1140
GGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAGGTTACCAACTACCTA
GlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThrAsnTyrLeu
      1150      1160      1170
GACTGGATTGCTGACAACATGCGACCGTGA - 3'
AspTrpIleArgAspAsnMetArgPro***

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Fig. 40. DNA sequence of coding region in pmSTTk
(Upper: Coding chain
Lower: Coded amino acid sequence)

```

5' - ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGGAGCAGTCTTCGTT
MetAspAlaMetLysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal
      10      20      30      40      50      60
TCGCCCAGCCAGGAAATCCATGCCCGATTGAGAAGAGGAGCCAGATCTGAGGGAACAGT
SerProSerGlnGluIleHisAlaArgPheArgArgGlyAlaArgSerGluGlyAsnSer
      70      80      90      100     110     120
GACTGCTACTTTGGGAATGGGTGAGCCTACCGTGGCAGCAGCAGCCTCAGCGAGTGGGT
AspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSerLeuThrGluSerGly
      130     140     150     160     170     180
GCCTCCTGCTCCCGTGGAAATCCATGATCCTGATAGGCAAGGTTTACACAGCACAGAAC
AlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysValTyrThrAlaGlnAsn
      190     200     210     220     230     240
CCCAGTGGCCAGGCACTGGGCTGGGCAACATAATTACTGCCGGAATCCTGATGGGGAT
ProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnProAspGlyAsp
      250     260     270     280     290     300
GCCAAGCCCTGGTGGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTG
AlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCysAspVal
      310     320     330     340     350     360
CCCTCCTGCTCCACCTGCGGCTGAGACAGTACAGCCAGCCACAGTTTGATATCAAAGGA
ProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheAspIleLysGly
      370     380     390     400     410     420
GGCCTCTTCGCGGACATCGCCTCCACCCCTGGCAGGCTGCCATCTTTGCCAAGCACAGG
GlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLysHisArg
      430     440     450     460     470     480
AGGTGCGCCGGAGAGCGGTTCTCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGATTCTC
ArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrpIleLeu
      490     500     510     520     530     540
TCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGC
SerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIleLeuGly
      550     560     570     580     590     600
AGAACATACCGGCTGCTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATT
ArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLysTyrIle
      610     620     630     640     650     660
GTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAA
ValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAlaLeuLeuGlnLeuLys
      670     680     690     700     710     720
TCGGATTCTGCGCGCTGTGCCAGGAGCAGCGTGGTCCGCACTGTGTGCTTCCCCCG
SerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCysLeuProPro
      730     740     750     760     770     780
GCGGACCTGGAGCTGCCGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAG
AlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGlyLysHisGlu
      790     800     810     820     830     840
GCCTTGCTCTCTTTCTATTGCGAGCGGCTGAAGGAGGCTCATGTGACAGTGTACCCATCC
AlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeuTyrProSer
      850     860     870     880     890     900
AGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCT
SerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMetLeuCysAla
      910     920     930     940     950     960
GGAGACACTCGGAGCGGGGCCCCAGGCAAACTTGCACGACGCTGCCAGGGCGATTG
GlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGlnGlyAspSer
      970     980     990    1000    1010    1020
GGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCTGG
GlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIleIleSerTrp
      1030    1040    1050    1060    1070    1080
GGCCTGGGCTGTGGACAGAAGGATGCCCCGGTGTGTACACAAAGGTTACCAACTACCTA
GlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThrAsnTyrLeu
      1090    1100    1110    1120    1130    1140
GACTGGATTCTGTGACAACATCGGACCGTGA - 3'
AspTrpIleArgAspAsnMetArgPro***
      1150    1160    1170

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POOR QUALITY



DOCUMENTS CONSIDERED TO BE RELEVANT			EP 88112569.4
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.4)
X	EP - A2 - 0 199 574 (GENENTECH, INC.) * Fig. 2B-2E; claims 1-4,7-9, 13-20 *	1-9	C 12 N 15/00 C 07 K 13/00 C 12 N 9/50 C 07 H 21/04 A 61 K 37/54
X	EP - A1 - 0 093 619 (GENENTECH, INC.) * Fig. 5; claims 1-7,9,11-15 *	1-9	
D,X	EP - A2 - 0 196 920 (BEECHAM GROUP PLC) * Claims 1,8,10,11 *	1-9, 12,13	
P,X	EP - A1 - 0 241 208 (BEECHAM GROUP PLC) * Claims 1-10,13-15,24 *	1-9, 12,13	TECHNICAL FIELDS SEARCHED (Int. Cl.4)
P,X	EP - A2 - 0 233 013 (BEECHAM GROUP PLC) * Claims 1-3,7,8,12 *	1-9, 13,14	C 12 N C 07 K C 07 H A 61 K
X	EP - A2 - 0 201 153 (BEECHAM GROUP PLC) * Claims 1-7,11,14 *	1-9	
The present search report has been drawn up for all claims			
Place of search VIENNA		Date of completion of the search 11-11-1988	Examiner WOLF
CATEGORY OF CITED DOCUMENTS			
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

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